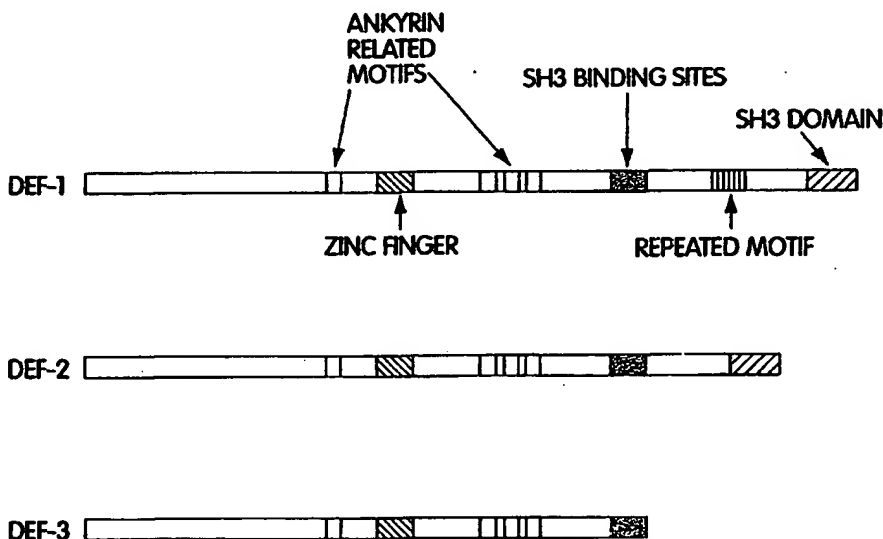




INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/46, 14/47, 14/475, C12N 15/11, C07K 16/22, A61K 38/18, C12N 15/62 // A01K 67/027, C12N 9/00, G01N 33/53</p>	<p>A1</p>	<p>(11) International Publication Number: WO 98/36065 (43) International Publication Date: 20 August 1998 (20.08.98)</p>
<p>(21) International Application Number: PCT/US98/02724 (22) International Filing Date: 13 February 1998 (13.02.98) (30) Priority Data: 60/038,191 14 February 1997 (14.02.97) US (71) Applicant: DANA-FARBER CANCER INSTITUTE [US/US]; 44 Binney Street, Boston, MA 02115 (US). (72) Inventors: THOMAS, Roberts, M.; 13 Berkeley Street, Cam- bridge, MA 02138 (US). KING, Frederick, J.; Apartment 22, 217 Kent Street, Brookline, MA 02146 (US). HARRIS, David, F.; 45 Robin Hood Drive, Gales Ferry, CT 06335 (US). HU, Erding; 709 Sweetland Road, King of Prussia, PA 19406 (US). SPIEGELMAN, Bruce; 271 Waban, Wa- ban, MA 02168 (US). CHAN, Joanne; Apartment 4, 82 St. Paul Street, Brookline, MA 02146 (US). (74) Agents: MANDRAGOURAS, Amy, E. et al.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).</p>	<p>(81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p>	

(54) Title: DIFFERENTIATION ENHANCING FACTORS AND USES THEREFOR



(57) Abstract

The present invention relates to novel SH3 domain binding protein, referred to herein as a DEF polypeptides. The DEF polypeptides comprise several motifs including a *src* SH3 consensus binding sequence, four ankyrin repeats, one zinc finger domain and six copies of a proline-rich tandem repeat. DEF polypeptides may function as mediators of SH3 domain-dependent signal transduction pathways and, thus may mediate multiple signaling events such as cellular gene expression, cytoskeletal architecture, protein trafficking and endocytosis, cell adhesion, migration, proliferation and differentiation. Described herein are isolated and antisense nucleic acids molecules, recombinant expression vectors, host cells and non-human transgenic animals containing an insertion or a disruption of the DEF gene. Diagnostic, screening and therapeutic methods utilizing the compositions of the invention are also provided.

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Met Glu Gly Glu Val Ile Val Val Thr Gly Glu Glu Asp Gln Glu Trp
 1090 1095 1100

5 Trp Ile Gly His Ile Glu Gly Gln Pro Glu Arg Lys Gly Val Phe Pro
 1105 1110 1115 1120

Val Ser Phe Val His Ile Leu Ser Asp
 1125

10 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 4382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 351..3803

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GACAAAAGCT GGAGCTCGCG CGCCTGCAGG TCGACACTAG TGGATCCAAA GAATTCGGCA 60
 30 CGAGCTCCGG CCCCCTCCAA ACTCACATGC CGGACTCCCG CTCCTGTCC AGCAGCTCCA 120
 GATGGGGCAG ATCAATGCGC GCATTCTGTC TCATTGTAAC TGTAGCGGCA TGTGATTTC 180
 35 GCCCGTAATG TCCGCGCGCT GGACGGAGCA CAATGCGCTG AATATGGTGC CACTCGGAAA 240
 CACGGAGCTG TACGCACAAT CTGCTTTGCA ATTACTTTTT AATCTGTAA TACGGAGTGA 300
 AACCGCAGCT GTCTCGCTCA GGGTTGTTTT GCTGAGGTGA CTACAGAGCC ATG AGG 356
 Met Arg
 40 1
 TCC TCG TCC TCG CGT TTG TCA AGT TTT TCC TCC AGG GAT TCA TTA TGG 404
 Ser Ser Ser Ser Arg Leu Ser Ser Phe Ser Ser Arg Asp Ser Leu Trp
 5 10 15
 45 AGT CGG ATG CCG GAT CAG ATC TCC GTG TCC GAG TTT CTC TCG GAG ACG 452
 Ser Arg Met Pro Asp Gln Ile Ser Val Ser Glu Phe Leu Ser Glu Thr
 20 25 30
 50 ACG GAG GAT TAC AAT TCC CCC ACG ACC TCG AGC TTC ACC ACC CGC CTG 500
 Thr Glu Asp Tyr Asn Ser Pro Thr Thr Ser Ser Phe Thr Thr Arg Leu
 35 40 45 50

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	CAG AGC TGC CGG AAC ACG GTC AAT GTT CTG GAA GAG GCT TTG GAT CAG	548
	Gln Ser Cys Arg Asn Thr Val Asn Val Leu Glu Glu Ala Leu Asp Gln	
	55 60 65	
5	GAC CGA ACT GCT TTA CAG AAG GTC AAG AAA TCT GTC AAA GCA ATC TAC	596
	Asp Arg Thr Ala Leu Gln Lys Val Lys Lys Ser Val Lys Ala Ile Tyr	
	70 75 80	
10	AAC TCG GGT CAA GAA CAT GTG CAG AAT GAA GAG AAT TAT GGA CAG GCA	644
	Asn Ser Gly Gln Glu His Val Gln Asn Glu Glu Asn Tyr Gly Gln Ala	
	85 90 95	
15	CTG GAC AAG TTT GGC AGC AAC TTC ATC AGC CGA GAT AAC TCT GAT CTG	692
	Leu Asp Lys Phe Gly Ser Asn Phe Ile Ser Arg Asp Asn Ser Asp Leu	
	100 105 110	
20	GGA ACA GCC TTC ATC AAG TTT TCT GGA CTT ATC AAA GAG CTG GCT GCT	740
	Gly Thr Ala Phe Ile Lys Phe Ser Gly Leu Ile Lys Glu Leu Ala Ala	
	115 120 125 130	
25	CTC CTC AAG AAC CTG CTC CAG AGC CTC AGC CAC AAC GTC ATC TTC ACC	788
	Leu Leu Lys Asn Leu Leu Gln Ser Leu Ser His Asn Val Ile Phe Thr	
	135 140 145	
30	CTG GAC TCT CTG CTC AAA GGA GAT CTA AAG GGA GTG AAG GGG GAC CTT	836
	Leu Asp Ser Leu Leu Lys Gly Asp Leu Lys Gly Val Lys Gly Asp Leu	
	150 155 160	
35	AAA AAG CCT TTC GAC AAG GCC TGG AAA GAC TAT GAA ACC AAG TTC ACA	884
	Lys Lys Pro Phe Asp Lys Ala Trp Lys Asp Tyr Glu Thr Lys Phe Thr	
	165 170 175	
40	AAG ATC GAG AAG GAG AAG AGA GAA CAT GCC AAG CAG CAC GGC ATG ATC	932
	Lys Ile Glu Lys Glu Lys Arg Glu His Ala Lys Gln His Gly Met Ile	
	180 185 190	
45	CGC ACA GAA ATC ACC GGC GCA GAG ATT GCA GAA GAG ATG GAG AAG GAG	980
	Arg Thr Glu Ile Thr Gly Ala Glu Ile Ala Glu Glu Met Glu Lys Glu	
	195 200 205 210	
50	CGG AGG ATC TTT CAG CTG CAG ATG TGT GAG TAC CTG ATC AAA GTC AAT	1028
	Arg Arg Ile Phe Gln Leu Gln Met Cys Glu Tyr Leu Ile Lys Val Asn	
	215 220 225	
55	GAG ATT AAG ACC AAG AAG GGA GTG GAT CTC CTC CAG AAT CTC ATC AAG	1076
	Glu Ile Lys Thr Lys Lys Gly Val Asp Leu Leu Gln Asn Leu Ile Lys	
	230 235 240	
60	TAT TAT CAT GCA CAG TGC AAT TTC TTC CAG GAT GGC TTG AAA ACT GCT	1124
	Tyr Tyr His Ala Gln Cys Asn Phe Phe Gln Asp Gly Leu Lys Thr Ala	
	245 250 255	
65	GAC AAG TTG AAG CAG TAT ATT GAA AAA TTA GCA GCT GAT CTT TAT AAT	1172
	Asp Lys Leu Lys Gln Tyr Ile Glu Lys Leu Ala Ala Asp Leu Tyr Asn	
	260 265 270	

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5	ATA AAA CAG ACT CAG GAT GAG GAG AAA AAA CAG CTC ACA GCT CTC AGA	1220
	Ile Lys Gln Thr Gln Asp Glu Glu Lys Lys Gln Leu Thr Ala Leu Arg	
	275 280 285 290	
10	GAC CTC ATC AAA TCT TCC TTA CAG CTG GAC CAG AAG GAG GAT TCT CAG	1268
	Asp Leu Ile Lys Ser Ser Leu Gln Leu Asp Gln Lys Glu Asp Ser Gln	
	295 300 305	
15	AGT AAG CAG AGC GGG TAC AGC ATG CAC CAG CTG CAG GGC AAT AAG GAG	1316
	Ser Lys Gln Ser Gly Tyr Ser Met His Gln Leu Gln Gly Asn Lys Glu	
	310 315 320	
20	TTT GGC AGT GAG AAG AAG GGC TAT CTC TTC AAG AAG AGT GAT GGG ATC	1364
	Phe Gly Ser Glu Lys Lys Gly Tyr Leu Phe Lys Lys Ser Asp Gly Ile	
	325 330 335	
25	CGT AAG GTG TGG CAG AGG AGG AAG TGC TCA GTG AAA AAT GGC ATC CTC	1412
	Arg Lys Val Trp Gln Arg Arg Lys Cys Ser Val Lys Asn Gly Ile Leu	
	340 345 350	
30	ACC ATC TCT CAT GCC ACA TCC AAC AGG CAG CCG GTG AGA CTG AAT CTG	1460
	Thr Ile Ser His Ala Thr Ser Asn Arg Gln Pro Val Arg Leu Asn Leu	
	355 360 365 370	
35	CTG ACC TGC CAG GTT AAA CCC AGT GGA GAG GAT AAG AAG TGC TTT GAC	1508
	Leu Thr Cys Gln Val Lys Pro Ser Gly Glu Asp Lys Lys Cys Phe Asp	
	375 380 385	
40	CTC ATC TCT CAT AAT CGA ACA TAT CAT TTC CAG GCA GAG GAC GAA CAG	1556
	Leu Ile Ser His Asn Arg Thr Tyr His Phe Gln Ala Glu Asp Glu Gln	
	390 395 400	
45	GAG TTT GTG ATA TGG ATC TCG GTG CTG ACT AAT AGT AAG GAG GAG GCT	1604
	Glu Phe Val Ile Trp Ile Ser Val Leu Thr Asn Ser Lys Glu Glu Ala	
	405 410 415	
50	CTG AAC ATG GCA TTT CGT GGG GAG CAG AGT GCT GGA GAT GAC AGT TTG	1652
	Leu Asn Met Ala Phe Arg Gly Glu Gln Ser Ala Gly Asp Asp Ser Leu	
	420 425 430	
55	GAG GAC TTG ACC AAA GCC ATC ATC GAG GAC GTG CTG CGC ATT CCT GGA	1700
	Glu Asp Leu Thr Lys Ala Ile Ile Glu Asp Val Leu Arg Ile Pro Gly	
	435 440 445 450	
60	AAC GAA GTC TGC TGT GAC TGT GGG GTT CCA GAG CCC AAA TGG TTA TCC	1748
	Asn Glu Val Cys Cys Asp Cys Gly Val Pro Glu Pro Lys Trp Leu Ser	
	455 460 465	
65	ACT AAC CTC GGC ATC CTG ACG TGC ATC GAG TGT TCA GGA ATC CAC AGG	1796
	Thr Asn Leu Gly Ile Leu Thr Cys Ile Glu Cys Ser Gly Ile His Arg	
	470 475 480	

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	GAA ATG GGA GTC CAT ATT TCG CGC ATC CAA TCC ATG GAG CTT GAC AAA	1844
	Glu Met Gly Val His Ile Ser Arg Ile Gln Ser Met Glu Leu Asp Lys	
	485 490 495	
5	CTT GGA ACC TCT GAA CTC TTG CTG GCT AAG AAC GTG GGC AAC AGT AGT	1892
	Leu Gly Thr Ser Glu Leu Leu Leu Ala Lys Asn Val Gly Asn Ser Ser	
	500 505 510	
10	TTC AAC GAA ATA TTA GAA GGG AAT CTG CCG AGT CCT TCA CCA AAG CCA	1940
	Phe Asn Glu Ile Leu Glu Gly Asn Leu Pro Ser Pro Ser Pro Lys Pro	
	515 520 525 530	
15	GCG CCA TCA AGT GAC ATG ACC GAG AGG AAG GAG TAC ATC AAT GCG AAG	1988
	Ala Pro Ser Ser Asp Met Thr Glu Arg Lys Glu Tyr Ile Asn Ala Lys	
	535 540 545	
20	TAC GTG GAG CAC AGG TTC GCT CGG CGA ACG GCC ACT ACA GCC ACA GCC	2036
	Tyr Val Glu His Arg Phe Ala Arg Arg Thr Ala Thr Thr Ala Thr Ala	
	550 555 560	
25	AGA CAG GGC GAC TTG TAC GAG GCG GTG AGA ACG CGA GAC TTG ATG GCT	2084
	Arg Gln Gly Asp Leu Tyr Glu Ala Val Arg Thr Arg Asp Leu Met Ala	
	565 570 575	
30	GAA GCA GGA CAG GAC CCG GGA GAG ACA GCT CTG CAC TTT GCT GTT CGG	2180
	Glu Ala Gly Gln Asp Pro Gly Glu Thr Ala Leu His Phe Ala Val Arg	
	595 600 605 610	
35	ACA TCA GAC CAG ACT TCC CTG CAC CTG GTG GAC TTT CTT GTC CAA AAC	2228
	Thr Ser Asp Gln Thr Ser Leu His Leu Val Asp Phe Leu Val Gln Asn	
	615 620 625	
40	AGT GGG ACT CTA GAC AGA CAG ACG GAG AGT GGA AAC GCT GCT CTC CAT	2276
	Ser Gly Thr Leu Asp Arg Gln Thr Glu Ser Gly Asn Ala Ala Leu His	
	630 635 640	
45	TAC TGC TGC ACA TAT GAG AAG CCA GAG TGT CTC AAA CTG CTG CTC AGG	2324
	Tyr Cys Cys Thr Tyr Glu Lys Pro Glu Cys Leu Lys Leu Leu Leu Arg	
	645 650 655	
50	GGA AAA CCG TCT ATT GAC CTG GTT AAT CAA AAC GGG GAG ACA GCA TTG	2372
	Gly Lys Pro Ser Ile Asp Leu Val Asn Gln Asn Gly Glu Thr Ala Leu	
	660 665 670	
50	GAT ATC GCC AGA CGA CTG AGA AAT GTA CAG TGT GAA GAG CTA CTG GTG	2420
	Asp Ile Ala Arg Arg Leu Arg Asn Val Gln Cys Glu Glu Leu Leu Val	
	675 680 685 690	

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	GAG GCA GCA GCC GGG AGG TTT AAT CCT CAT GTG CAT GTG GAG TAT GAG	2468
	Glu Ala Ala Ala Gly Arg Phe Asn Pro His Val His Val Glu Tyr Glu	
	695 700 705	
5	TGG AAT CTG CGG CTG GAG GAG ATT GAT GAG AGT GAC GAT GAC CTG GAT	2516
	Trp Asn Leu Arg Leu Glu Glu Ile Asp Glu Ser Asp Asp Asp Leu Asp	
	710 715 720	
10	GAC AAG CCT AGT CCA GTG AAG AAG GAG CGT TCT CCT CGT CCT CAG AGC	2564
	Asp Lys Pro Ser Pro Val Lys Lys Glu Arg Ser Pro Arg Pro Gln Ser	
	725 730 735	
15	TTC TGT CAT TCG TCC AGC GTG TCT CCT CAG GAG AAG TTA ACC CTG CCG	2612
	Phe Cys His Ser Ser Ser Val Ser Pro Gln Glu Lys Leu Thr Leu Pro	
	740 745 750	
20	GGG TAT CTA GGA CAC AGG GAC AAG CAG AGA CTG TCC TAT GGA GCC TTT	2660
	Gly Tyr Leu Gly His Arg Asp Lys Gln Arg Leu Ser Tyr Gly Ala Phe	
	755 760 765 770	
25	GCC AAC CCC GTC TAC AGC ACC TCC ACC GAA ACC CCT GCA TCT CCA GTG	2708
	Ala Asn Pro Val Tyr Ser Thr Ser Thr Glu Thr Pro Ala Ser Pro Val	
	775 780 785	
30	TGT GGG CCG CCC ACC TCT CTG CCG CTG GGA TCT CAA TCG AGT GCA GGA	2804
	Cys Gly Pro Pro Thr Ser Leu Pro Leu Gly Ser Gln Ser Ser Ala Gly	
	805 810 815	
35	GGC AGC TCC ACT TTG TCT AAG AAG AGA GCT CCT CCT CCA CCT CCC GGA	2852
	Gly Ser Ser Thr Leu Ser Ser Lys Lys Arg Ala Pro Pro Pro Pro Gly	
	820 825 830	
40	CAC AAG CGC ACC CAC TCA GAT CCC CCC AGT CCC GTA CTG CAG GGT CCG	2900
	His Lys Arg Thr His Ser Asp Pro Pro Ser Pro Val Leu Gln Gly Pro	
	835 840 845 850	
45	CAG AGC AAA GGA AGT GAG TCC ACA CCT CCT TCT GCA AAT CGG ACA TCC	2948
	Gln Ser Lys Gly Ser Glu Ser Thr Pro Pro Ser Ala Asn Arg Thr Ser	
	855 860 865	
50	CCG GCC AAC AAG TTT GAG GGA ATC CAG CAG CAG CAA AGC ACT ACG TCT	2996
	Pro Ala Asn Lys Phe Glu Gly Ile Gln Gln Gln Gln Ser Thr Thr Ser	
	870 875 880	
55	ATG AAC ACA AAA GCA ACA TTT GGC CCA CGA GTT CTT CCC AAA CTA CCT	3044
	Met Asn Thr Lys Ala Thr Phe Gly Pro Arg Val Leu Pro Lys Leu Pro	
	885 890 895	
55	CAA AAA GTG GCA CTA CGA AAG ATT GAC ACA ATC CAC CTC CCA TCA GTG	3092
	Gln Lys Val Ala Leu Arg Lys Ile Asp Thr Ile His Leu Pro Ser Val	
	900 905 910	

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5	GAC AAG TCT GGT CCT GAT GTG CTT CAG AAA CCC CCA CAG GCC CAG GAT	3140
	Asp Lys Ser Gly Pro Asp Val Leu Gln Lys Pro Pro Gln Ala Gln Asp	
	915 920 925 930	
10	GCA CCT CCC ACC AGA GCC TCA GAT ACA ATA ACC AGA CCC ACT GAA CCT	3188
	Ala Pro Pro Thr Arg Ala Ser Asp Thr Ile Thr Arg Pro Thr Glu Pro	
	935 940 945	
15	CCA CCT AAA ATT CCA CAG GTC GCA GAA CGA TCC CAG CCT GTG GAT GTC	3236
	Pro Pro Lys Ile Pro Gln Val Ala Glu Arg Ser Gln Pro Val Asp Val	
	950 955 960	
20	CCG CAG AAA CCG CAC ATC TCA GAC CTT CCT CCC AAA CCG CAA CTA TCA	3284
	Pro Gln Lys Pro His Ile Ser Asp Leu Pro Pro Lys Pro Gln Leu Ser	
	965 970 975	
25	GAT CTT CCC CCC AAA CCC CAA TTG TCG GAT TTA CCA CCA AAA CCT CAG	3332
	Asp Leu Pro Pro Lys Pro Gln Leu Ser Asp Leu Pro Pro Lys Pro Gln	
	980 985 990	
30	CTT TCT GAC CTG CCC CCG AAG CCT CAG CTT AAG GAT CTT CCC CCT AAG	3380
	Leu Ser Asp Leu Pro Pro Lys Pro Gln Leu Lys Asp Leu Pro Pro Lys	
	995 1000 1005 1010	
35	CCG CAG ATC AGT GAT CTG CCA TCC AAA CCG GCC GTG TGT TCT GCG TCT	3428
	Pro Gln Ile Ser Asp Leu Pro Ser Lys Pro Ala Val Cys Ser Ala Ser	
	1015 1020 1025	
40	GAG GCC ACA CAG AGG CAG TCA ACG CAG GAG GAA ACC AGT CCG AAG CCC	3476
	Glu Ala Thr Gln Arg Gln Ser Thr Gln Glu Glu Thr Ser Pro Lys Pro	
	1030 1035 1040	
45	CAG CTG ACG GAG ACA CAG TCA TTC AGC CAG CAG GAG GAG CTC TCA CCC	3524
	Gln Leu Thr Glu Thr Gln Ser Phe Ser Gln Gln Glu Glu Leu Ser Pro	
	1045 1050 1055	
50	CGA CAG GCC AGC GAG GAC ACC AAT GGA GCG CCC GCA GGA GCC TTG GAA	3572
	Arg Gln Ala Ser Glu Asp Thr Asn Gly Ala Pro Ala Gly Ala Leu Glu	
	1060 1065 1070	
55	ATG CCA GTC CCA ATG CCA CGC AAA ATT AAC ACA GTA GCA AAG AAC AAA	3620
	Met Pro Val Pro Met Pro Arg Lys Ile Asn Thr Val Ala Lys Asn Lys	
	1075 1080 1085 1090	
60	GCG AAG CGT GTG AAA ACC ATC TAT GAT TGC CAG GCA GAC AAT GAC GAT	3668
	Ala Lys Arg Val Lys Thr Ile Tyr Asp Cys Gln Ala Asp Asn Asp Asp	
	1095 1100 1105	
65	GAG CTG ACT TTT GTG GAG GGC GAG GTT ATA ATT GTC ACA GGA GAG GAA	3716
	Glu Leu Thr Phe Val Glu Gly Glu Val Ile Ile Val Thr Gly Glu Glu	
	1110 1115 1120	

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GAC CAG GAG TGG TGG ATC GGG CAC ATA GAG GGT CAG CCT GAA AGG AAA 3764
 Asp Gln Glu Trp Trp Ile Gly His Ile Glu Gly Gln Pro Glu Arg Lys
 1125 1130 1135

5 GGG GTC TTC CCA ATG TCC TTC GTG CAC ATT CTG TCA GAC TGACAGTGCA 3813
 Gly Val Phe Pro Met Ser Phe Val His Ile Leu Ser Asp
 1140 1145 1150

10 TGACCGGCAG CCGAGAGGCT CTCTAACTAG CACAAGCTCC GCTCTCTCTG GCCTCACACT 3873
 GGACTGTGGG CATTGCCTCT GTACATAGCT GCTGAAACCC AAACGGTCTC CAAACACATA 3933
 CAAAACTGAA GTATCAAACC CATGCTCCCT TAATCCTCAA GGGTGAAATG TGTAACTAT 3993

15 GTGTTGTTC TAAACTGTGT TATCCTGCCT ACCAGTATTA TCGTAGCCAT GGCAGCCCAG 4053
 CATGCCATA CTGGGTTTGC AGTAGCTATA CTTGGAAATC TAGCACTTAA CATGTATGCT 4113
 GTAACCTTGT GTATGTGTAC ACATATAGAA TTATATGTAT GTCCATTTTA AGTGTGTCTT 4173

20 TGTACATACA TATGCACAGA CGTAAGTGTA TATTTATGTA CGTATGTATA ATGTACAAGT 4233
 GTGCAAATGT ATGTTAACCC TGCTTGCTTA TGGAGCCAGA GTGACTCTAG ACATTTTAGT 4293

25 GTACTGTTTT AAAAAAAAAA AAAAAAAAAAC TCGAGAGTAC TTCTAGAGCG GCCGCGGGCC 4353
 CATCGATTTT CCACCCGGGT GGGGTACCA 4382

30 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1151 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 Met Arg Ser Ser Ser Ser Arg Leu Ser Ser Phe Ser Ser Arg Asp Ser
 1 5 10 15

45 Leu Trp Ser Arg Met Pro Asp Gln Ile Ser Val Ser Glu Phe Leu Ser
 20 25 30

Glu Thr Thr Glu Asp Tyr Asn Ser Pro Thr Thr Ser Ser Phe Thr Thr
 35 40 45

50 Arg Leu Gln Ser Cys Arg Asn Thr Val Asn Val Leu Glu Glu Ala Leu
 50 55 60

Asp Gln Asp Arg Thr Ala Leu Gln Lys Val Lys Lys Ser Val Lys Ala
 65 70 75 80

55

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[illegible]

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	Asn	Leu	Leu	Thr	Cys	Gln	Val	Lys	Pro	Ser	Gly	Glu	Asp	Lys	Lys	Cys	370	375	380
5	Phe	Asp	Leu	Ile	Ser	His	Asn	Arg	Thr	Tyr	His	Phe	Gln	Ala	Glu	Asp	385	390	395
	Glu	Gln	Glu	Phe	Val	Ile	Trp	Ile	Ser	Val	Leu	Thr	Asn	Ser	Lys	Glu	405	410	415
10	Glu	Ala	Leu	Asn	Met	Ala	Phe	Arg	Gly	Glu	Gln	Ser	Ala	Gly	Asp	Asp	420	425	430
	Ser	Leu	Glu	Asp	Leu	Thr	Lys	Ala	Ile	Ile	Glu	Asp	Val	Leu	Arg	Ile	435	440	445
15	Pro	Gly	Asn	Glu	Val	Cys	Cys	Asp	Cys	Gly	Val	Pro	Glu	Pro	Lys	Trp	450	455	460
	Leu	Ser	Thr	Asn	Leu	Gly	Ile	Leu	Thr	Cys	Ile	Glu	Cys	Ser	Gly	Ile	465	470	475
20	His	Arg	Glu	Met	Gly	Val	His	Ile	Ser	Arg	Ile	Gln	Ser	Met	Glu	Leu	485	490	495
25	Asp	Lys	Leu	Gly	Thr	Ser	Glu	Leu	Leu	Leu	Ala	Lys	Asn	Val	Gly	Asn	500	505	510
	Ser	Ser	Phe	Asn	Glu	Ile	Leu	Glu	Gly	Asn	Leu	Pro	Ser	Pro	Ser	Pro	515	520	525
30	Lys	Pro	Ala	Pro	Ser	Ser	Asp	Met	Thr	Glu	Arg	Lys	Glu	Tyr	Ile	Asn	530	535	540
	Ala	Lys	Tyr	Val	Glu	His	Arg	Phe	Ala	Arg	Arg	Thr	Ala	Thr	Thr	Ala	545	550	555
35	Thr	Ala	Arg	Gln	Gly	Asp	Leu	Tyr	Glu	Ala	Val	Arg	Thr	Arg	Asp	Leu	565	570	575
40	Met	Ala	Leu	Ile	Gln	Leu	Tyr	Ala	Asp	Gly	Val	Glu	Leu	Met	Asp	Pro	580	585	590
	Phe	Pro	Glu	Ala	Gly	Gln	Asp	Pro	Gly	Glu	Thr	Ala	Leu	His	Phe	Ala	595	600	605
45	Val	Arg	Thr	Ser	Asp	Gln	Thr	Ser	Leu	His	Leu	Val	Asp	Phe	Leu	Val	610	615	620
	Gln	Asn	Ser	Gly	Thr	Leu	Asp	Arg	Gln	Thr	Glu	Ser	Gly	Asn	Ala	Ala	625	630	635
50	Leu	His	Tyr	Cys	Cys	Thr	Tyr	Glu	Lys	Pro	Glu	Cys	Leu	Lys	Leu	Leu	645	650	655

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Leu Arg Gly Lys Pro Ser Ile Asp Leu Val Asn Gln Asn Gly Glu Thr
 660 665 670

5 Ala Leu Asp Ile Ala Arg Arg Leu Arg Asn Val Gln Cys Glu Glu Leu
 675 680 685

Leu Val Glu Ala Ala Ala Gly Arg Phe Asn Pro His Val His Val Glu
 690 695 700

10 Tyr Glu Trp Asn Leu Arg Leu Glu Glu Ile Asp Glu Ser Asp Asp Asp
 705 710 715 720

Leu Asp Asp Lys Pro Ser Pro Val Lys Lys Glu Arg Ser Pro Arg Pro
 725 730 735

15 Gln Ser Phe Cys His Ser Ser Ser Val Ser Pro Gln Glu Lys Leu Thr
 740 745 750

20 Leu Pro Gly Tyr Leu Gly His Arg Asp Lys Gln Arg Leu Ser Tyr Gly
 755 760 765

Ala Phe Ala Asn Pro Val Tyr Ser Thr Ser Thr Glu Thr Pro Ala Ser
 770 775 780

25 Pro Val Ser Glu Gly Pro Thr Ile Ala Ser Lys Thr Pro Ala Lys Ala
 785 790 795 800

Pro Ser Cys Gly Pro Pro Thr Ser Leu Pro Leu Gly Ser Gln Ser Ser
 805 810 815

30 Ala Gly Gly Ser Ser Thr Leu Ser Lys Lys Arg Ala Pro Pro Pro Pro
 820 825 830

35 Pro Gly His Lys Arg Thr His Ser Asp Pro Pro Ser Pro Val Leu Gln
 835 840 845

Gly Pro Gln Ser Lys Gly Ser Glu Ser Thr Pro Pro Ser Ala Asn Arg
 850 855 860

40 Thr Ser Pro Ala Asn Lys Phe Glu Gly Ile Gln Gln Gln Gln Ser Thr
 865 870 875 880

Thr Ser Met Asn Thr Lys Ala Thr Phe Gly Pro Arg Val Leu Pro Lys
 885 890 895

45 Leu Pro Gln Lys Val Ala Leu Arg Lys Ile Asp Thr Ile His Leu Pro
 900 905 910

Ser Val Asp Lys Ser Gly Pro Asp Val Leu Gln Lys Pro Pro Gln Ala
 915 920 925

50 Gln Asp Ala Pro Pro Thr Arg Ala Ser Asp Thr Ile Thr Arg Pro Thr
 930 935 940

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Glu Pro Pro Pro Lys Ile Pro Gln Val Ala Glu Arg Ser Gln Pro Val
 945 950 955 960
 5 Asp Val Pro Gln Lys Pro His Ile Ser Asp Leu Pro Pro Lys Pro Gln
 965 970 975
 Leu Ser Asp Leu Pro Pro Lys Pro Gln Leu Ser Asp Leu Pro Pro Lys
 980 985 990
 10 Pro Gln Leu Ser Asp Leu Pro Pro Lys Pro Gln Leu Lys Asp Leu Pro
 995 1000 1005
 Pro Lys Pro Gln Ile Ser Asp Leu Pro Ser Lys Pro Ala Val Cys Ser
 1010 1015 1020
 15 Ala Ser Glu Ala Thr Gln Arg Gln Ser Thr Gln Glu Glu Thr Ser Pro
 1025 1030 1035 1040
 Lys Pro Gln Leu Thr Glu Thr Gln Ser Phe Ser Gln Gln Glu Glu Leu
 20 1045 1050 1055
 Ser Pro Arg Gln Ala Ser Glu Asp Thr Asn Gly Ala Pro Ala Gly Ala
 1060 1065 1070
 25 Leu Glu Met Pro Val Pro Met Pro Arg Lys Ile Asn Thr Val Ala Lys
 1075 1080 1085
 Asn Lys Ala Lys Arg Val Lys Thr Ile Tyr Asp Cys Gln Ala Asp Asn
 1090 1095 1100
 30 Asp Asp Glu Leu Thr Phe Val Glu Gly Glu Val Ile Ile Val Thr Gly
 1105 1110 1115 1120
 Glu Glu Asp Gln Glu Trp Trp Ile Gly His Ile Glu Gly Gln Pro Glu
 35 1125 1130 1135
 Arg Lys Gly Val Phe Pro Met Ser Phe Val His Ile Leu Ser Asp
 1140 1145 1150

40 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3456 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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ATGAGGTCCT CGTCCTCGCG TTTGTCAAGT TTTTCCTCCA GGGATTCATT ATGGAGTCGG 60

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	ATGCCGGATC AGATCTCCGT GTCCGAGTTT CTCTCGGAGA CGACGGAGGA TTACAATTCC	120
	CCCACGACCT CGAGCTTCAC CACCCGCCTG CAGAGCTGCC GGAACACGGT CAATGTTCTG	180
5	GAAGAGGCTT TGGATCAGGA CCGAACTGCT TTACAGAAGG TCAAGAAATC TGTCAAAGCA	240
	ATCTACAACT CGGGTCAAGA ACATGTGCAG AATGAAGAGA ATTATGGACA GGCCTGGAC	300
	AAGTTTGGCA GCAACTTCAT CAGCCGAGAT AACTCTGATC TGGGAACAGC CTTTCATCAAG	360
10	TTTTCTGGAC TTATCAAAGA GCTGGCTGCT CTCCTCAAGA ACCTGCTCCA GAGCCTCAGC	420
	CACAACGTCA TCTTCACCCT GGACTCTCTG CTCAAAGGAG ATCTAAAGGG AGTGAAGGGG	480
15	GACCTTAAAA AGCCTTTTCGA CAAGGCCTGG AAAGACTATG AAACCAAGTT CACAAAGATC	540
	GAGAAGGAGA AGAGAGAACA TGCCAAGCAG CACGGCATGA TCCGCACAGA AATCACCGGC	600
	GCAGAGATTG CAGAAGAGAT GGAGAAGGAG CGGAGGATCT TTCAGCTGCA GATGTGTGAG	660
20	TACCTGATCA AAGTCAATGA GATTAAGACC AAGAAGGGAG TGGATCTCCT CCAGAATCTC	720
	ATCAAGTATT ATCATGCACA GTGCAATTTT TTCCAGGATG GCTTGAAAAC TGCTGACAAG	780
25	TTGAAGCAGT ATATTGAAAA ATTAGCAGCT GATCTTTATA ATATAAAACA GACTCAGGAT	840
	GAGGAGAAAA AACAGCTCAC AGCTCTCAGA GACCTCATCA AATCTTCCTT ACAGCTGGAC	900
	CAGAAGGAGG ATTCTCAGAG TAAGCAGAGC GGGTACAGCA TGCACCAGCT GCAGGGCAAT	960
30	AAGGAGTTTG GCAGTGAGAA GAAGGGCTAT CTCTTCAAGA AGAGTGATGG GATCCGTAAG	1020
	GTGTGGCAGA GGAGGAAGTG CTCAGTGAAA AATGGCATCC TCACCATCTC TCATGCCACA	1080
35	TCCAACAGGC AGCCGGTGAG ACTGAATCTG CTGACCTGCC AGGTTAAACC CAGTGGAGAG	1140
	GATAAGAAGT GCTTTGACCT CATCTCTCAT AATCGAACAT ATCATTTCCA GGCAGAGGAC	1200
	GAACAGGAGT TTGTGATATG GATCTCGGTG CTGACTAATA GTAAGGAGGA GGCTCTGAAC	1260
40	ATGGCATTTC GTGGGGAGCA GAGTGCTGGA GATGACAGTT TGGAGGACTT GACCAAAGCC	1320
	ATCATCGAGG ACGTGCTGCG CATTCCTGGA AACGAAGTCT GCTGTGACTG TGGGGTTCCA	1380
45	GAGCCCAAAT GGTATCCAC TAACCTCGGC ATCCTGACGT GCATCGAGTG TTCAGGAATC	1440
	CACAGGGAAA TGGGAGTCCA TATTTGCGCG ATCCAATCCA TGGAGCTTGA CAAACTTGGA	1500
	ACCTCTGAAC TCTTGCTGGC TAAGAACGTG GGCAACAGTA GTTTCAACGA AATATTAGAA	1560
50	GGGAATCTGC CGAGTCCTTC ACCAAAGCCA GCGCCATCAA GTGACATGAC CGAGAGGAAG	1620
	GAGTACATCA ATGCGAAGTA CGTGGAGCAC AGGTTTCGCTC GGCGAACGGC CACTACAGCC	1680
55	ACAGCCAGAC AGGGCGACTT GTACGAGGCG GTGAGAACGC GAGACTTGAT GGCTCTCATT	1740

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	CAGCTCTATG	CAGATGGAGT	GGAGCTAATG	GATCCTTTCC	CAGAAGCAGG	ACAGGACCCG	1800
	GGAGAGACAG	CTCTGCACTT	TGCTGTTCCG	ACATCAGACC	AGACTTCCCT	GCACCTGGTG	1860
5	GACTTTCTTG	TCCAAAACAG	TGGGACTCTA	GACAGACAGA	CGGAGAGTGG	AAACGCTGCT	1920
	CTCCATTACT	GCTGCACATA	TGAGAAGCCA	GAGTGTCTCA	AACTGCTGCT	CAGGGGAAAA	1980
10	CCGTCTATTG	ACCTGGTTAA	TCAAAACGGG	GAGACAGCAT	TGGATATCGC	CAGACGACTG	2040
	AGAAATGTAC	AGTGTGAAGA	GCTACTGGTG	GAGGCAGCAG	CCGGGAGGTT	TAATCCTCAT	2100
	GTGCATGTGG	AGTATGAGTG	GAATCTGCGG	CTGGAGGAGA	TTGATGAGAG	TGACGATGAC	2160
15	CTGGATGACA	AGCCTAGTCC	AGTGAAGAAG	GAGCGTTCTC	CTCGTCCTCA	GAGCTTCTGT	2220
	CATTCGTCCA	GCGTGTCTCC	TCAGGAGAAG	TTAACCCTGC	CGGGGTATCT	AGGACACAGG	2280
20	GACAAGCAGA	GACTGTCCTA	TGGAGCCTTT	GCCAACCCCG	TCTACAGCAC	CTCCACCGAA	2340
	ACCCCTGCAT	CTCCAGTGTC	AGAGGGACCC	ACCATAGCCA	GCAAGACCCC	TGCAAAAGCT	2400
	CCGTCCTGTG	GGCCGCCCAC	CTCTCTGCCG	CTGGGATCTC	AATCGAGTGC	AGGAGGCAGC	2460
25	TCCACTTTGT	CTAAGAAGAG	AGCTCCTCCT	CCACCTCCCG	GACACAAGCG	CACCCACTCA	2520
	GATCCCCCCA	GTCCCGTACT	GCAGGGTCCG	CAGAGCAAAG	GAAGTGAGTC	CACACCTCCT	2580
30	TCTGCAAATC	GGACATCCCC	GGCCAACAAG	TTTGAGGGAA	TCCAGCAGCA	GCAAAGCACT	2640
	ACGTCTATGA	ACACAAAAGC	AACATTTGGC	CCACGAGTTC	TTCCCAAAC	ACCTCAAAAA	2700
	GTGGCACTAC	GAAAGATTGA	CACAATCCAC	CTCCCATCAG	TGGACAAGTC	TGGTCCTGAT	2760
35	GTGCTTCAGA	AACCCCCACA	GGCCCAGGAT	GCACCTCCCA	CCAGAGCCTC	AGATACAATA	2820
	ACCAGACCCA	CTGAACCTCC	ACCTAAAATT	CCACAGGTCG	CAGAACGATC	CCAGCCTGTG	2880
40	GATGTCCCGC	AGAAACCGCA	CATCTCAGAC	CTTCCTCCCA	AACCGCAACT	ATCAGATCTT	2940
	CCCCCCTAAC	CCCAATTGTC	GGATTTACCA	CCAAAACCTC	AGCTTTCTGA	CCTGCCCCCG	3000
	AAGCCTCAGC	TTAAGGATCT	TCCCCCTAAG	CCGCAGATCA	GTGATCTGCC	ATCCAAACCG	3060
45	GCCGTGTGTT	CTGCGTCTGA	GGCCACACAG	AGGCAGTCAA	CGCAGGAGGA	AACCAGTCCG	3120
	AAGCCCCAGC	TGACGGAGAC	ACAGTCATTG	AGCCAGCAGG	AGGAGCTCTC	ACCCCGACAG	3180
50	GCCAGCGAGG	ACACCAATGG	AGCGCCCGCA	GGAGCCTTGG	AAATGCCAGT	CCCAATGCCA	3240
	CGCAAAATTA	ACACAGTAGC	AAAGAACAAA	GCGAAGCGTG	TGAAAACCAT	CTATGATTGC	3300
55	CAGGCAGACA	ATGACGATGA	GCTGACTTTT	GTGGAGGGCG	AGGTTATAAT	TGTCACAGGA	3360

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GAGGAAGACC AGGAGTGGTG GATCGGGCAC ATAGAGGGTC AGCCTGAAAG GAAAGGGGTC 3420

TTCCCAATGT CCTTCGTGCA CATTCTGTCA GACTGA 3456

5 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 5954 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 433..3378

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAGCTCGCG CGCCTGCAGG TCGACACTAG TGGATCCAAA GAATTCGGCA CGAGGCAAAA 60
 25 TCCAGCACGA CAACCTACAC TCCTGTCCCA AAACAGAAGA GAAGCACATC ACCGCACTGC 120
 TTTATTATCA AACGAGTGGG CTAAATTCCT ACTTAACTG GAAGAAGTGA GATCCGTGAA 180
 AGAAAGAGAG GGAAAAAGAG AGAGATTTCC CCGTCGTACA AGCCGCACTT CAGTGTAGTT 240
 30 GGCTAATGAT TTGTATTAAT TCCCAACTTG TTTTAATCCA CCGAGGACAA AACACCGCGA 300
 TGATAAGACT CCAGGACGCT CATGAGAGTT TTAATTCGGC GTTTCATCTC TGAATTTCGA 360
 35 CATTAAGTGC ACCGCGACCG GCCAAATCAA GGATTAAACA CGACATTTGT GGATTTGCCC 420
 AAAGGAGATA CA ATG CCT GAC CAG ATA ACA GTG GCG GAG TTT GTC ACG 468
 Met Pro Asp Gln Ile Thr Val Ala Glu Phe Val Thr
 1 5 10
 40 GAG ACA AAT GAA GAT TAT AAA TCG CCC ACC GCC TCA AAC TTC ACC ACC 516
 Glu Thr Asn Glu Asp Tyr Lys Ser Pro Thr Ala Ser Asn Phe Thr Thr
 15 20 25
 45 AGA ATG ACT CAC TGC AGG AAC ACA GTA TCC GCA CTG GAG GAG GCC CTG 564
 Arg Met Thr His Cys Arg Asn Thr Val Ser Ala Leu Glu Glu Ala Leu
 30 35 40
 50 GAT GTG GAC CGC AGT GTC CTT TAC AAG ATG AAG AAG TCA GTT AAG GCT 612
 Asp Val Asp Arg Ser Val Leu Tyr Lys Met Lys Lys Ser Val Lys Ala
 45 50 55 60
 ATT TAC GCC TCG GGT CTG GCT CAT GTG GAG AAT GAG GAG CAG TAC ACT 660
 Ile Tyr Ala Ser Gly Leu Ala His Val Glu Asn Glu Glu Gln Tyr Thr
 55 65 70 75

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	CAA GCT CTG GAG AAG TTC GCA GAG AAC TGT GTG TAC AGA GAT GAC CCG	708
	Gln Ala Leu Glu Lys Phe Gly Glu Asn Cys Val Tyr Arg Asp Asp Pro	
	80 85 90	
5	GAC CTG GGA TCA GCC TTC CTG AAG TTC TCC GTC TTC ACC AAG GAG CTC	756
	Asp Leu Gly Ser Ala Phe Leu Lys Phe Ser Val Phe Thr Lys Glu Leu	
	95 100 105	
10	ACG GCA CTC TTC AAG AAC CTG TTT CAG AAC ATG AAT AAT ATC ATT ACC	804
	Thr Ala Leu Phe Lys Asn Leu Phe Gln Asn Met Asn Asn Ile Ile Thr	
	110 115 120	
15	TTC CCA TTG GAC AGT CTG CTG AAG GGA GAT CTG AAA GGG GTT AAA GGG	852
	Phe Pro Leu Asp Ser Leu Leu Lys Gly Asp Leu Lys Gly Val Lys Gly	
	125 130 135 140	
20	GAT CTC AAG AAG CCC TTC GAT AAA GCC TGG AAA GAC TAC GAG ACT AAA	900
	Asp Leu Lys Lys Pro Phe Asp Lys Ala Trp Lys Asp Tyr Glu Thr Lys	
	145 150 155	
25	GTC TCT AAA ATA GAG AAG GAG AAA AAA GAG CAC GCC CGG CAG CAC GGA	948
	Val Ser Lys Ile Glu Lys Glu Lys Lys Glu His Ala Arg Gln His Gly	
	160 165 170	
30	ATG ATC CGG ACG GAG ATC AGC GGA GCA GAG ATA GCA GAA GAG ATG GAA	996
	Met Ile Arg Thr Glu Ile Ser Gly Ala Glu Ile Ala Glu Glu Met Glu	
	175 180 185	
35	AAA GAG CGG CGT TTC TTC CAG CTT CAG ATG TGT GAG TAC CTC CTC AAA	1044
	Lys Glu Arg Arg Phe Phe Gln Leu Gln Met Cys Glu Tyr Leu Leu Lys	
	190 195 200	
40	GTC AAT GAA ATC AAG ATC AAA AAA GGT GTC GAC CTG CTC CAG AAT CTC	1092
	Val Asn Glu Ile Lys Ile Lys Lys Gly Val Asp Leu Leu Gln Asn Leu	
	205 210 215 220	
45	ATC AAA TAC TTC CAC GCA CAG TGC AAC TTC TTT CAG GAT GGT CTC AAA	1140
	Ile Lys Tyr Phe His Ala Gln Cys Asn Phe Phe Gln Asp Gly Leu Lys	
	225 230 235	
50	GCG GTG GAC AAC CTC AAA CCC TCA ATA GAA AAA CTG GCC ACA GAC TTG	1188
	Ala Val Asp Asn Leu Lys Pro Ser Ile Glu Lys Leu Ala Thr Asp Leu	
	240 245 250	
55	CAC TCG ATC AAA CAG GTA CAG GAT GAA GAA CGC AGA CAG CTA ACC CAG	1236
	His Ser Ile Lys Gln Val Gln Asp Glu Glu Arg Arg Gln Leu Thr Gln	
	255 260 265	
60	TTA CGG GAT GTG CTA AAA ACT GCT CTG CAA GTG GAG CAG AAG GAG GAC	1284
	Leu Arg Asp Val Leu Lys Thr Ala Leu Gln Val Glu Gln Lys Glu Asp	
	270 275 280	

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	TCT CAG GTT AGA CAG AGC GCC ACC TAC AGT CTG CAC CAG CCG CAG GGC	1332
	Ser Gln Val Arg Gln Ser Ala Thr Tyr Ser Leu His Gln Pro Gln Gly	
	285 290 295 300	
5	AAC AAA GAG CAT GGG ACT GAG CGC AGC GGC AAC CTT TAC AAG AAG AGT	1380
	Asn Lys Glu His Gly Thr Glu Arg Ser Gly Asn Leu Tyr Lys Lys Ser	
	305 310 315	
10	GAC GGG CTG CGG AAA GTG TGG CAG AAG AGA AAG TGC ACA GTA AAG AAT	1428
	Asp Gly Leu Arg Lys Val Trp Gln Lys Arg Lys Cys Thr Val Lys Asn	
	320 325 330	
15	GGA TAT TTG ACC ATC TCA CAT GGG ACG GCA AAC AGA CCT CCC GCC AAA	1476
	Gly Tyr Leu Thr Ile Ser His Gly Thr Ala Asn Arg Pro Pro Ala Lys	
	335 340 345	
20	CTC AAT CTT CTC ACC TGT CAG GTG AAG CAC AAC CCA GAG GAG AAG AAA	1524
	Leu Asn Leu Leu Thr Cys Gln Val Lys His Asn Pro Glu Glu Lys Lys	
	350 355 360	
25	AGT TTT GAC CTC ATC TCA CAT GAC AGA ACA TAT CAT TTC CAG GCA GAA	1572
	Ser Phe Asp Leu Ile Ser His Asp Arg Thr Tyr His Phe Gln Ala Glu	
	365 370 375 380	
30	GAT GAG CCA GAG TGT CAA ATA TGG ATC TCA GTG CTG CAG AAC AGT AAA	1620
	Asp Glu Pro Glu Cys Gln Ile Trp Ile Ser Val Leu Gln Asn Ser Lys	
	385 390 395	
35	GAA GAG GCG CTC AAC AAC GCC TTC AAG GGC GAC CAG CAT GTT GGT GAA	1668
	Glu Glu Ala Leu Asn Asn Ala Phe Lys Gly Asp Gln His Val Gly Glu	
	400 405 410	
40	AAT AAC ATT GTG CAG GAG CTC ACC AAG GCC ATC CTG GGA GAG GTG AAG	1716
	Asn Asn Ile Val Gln Glu Leu Thr Lys Ala Ile Leu Gly Glu Val Lys	
	415 420 425	
45	CGG ATG GCG GGG AAC GAT GTC TGC TGC GAC TGC GGT GCT CCC GGC CCC	1764
	Arg Met Ala Gly Asn Asp Val Cys Cys Asp Cys Gly Ala Pro Gly Pro	
	430 435 440	
50	ACA TGG CTC TCC ACC AAC CTG GGC ATC CTG ACC TGC ATC GAG TGT TCG	1812
	Thr Trp Leu Ser Thr Asn Leu Gly Ile Leu Thr Cys Ile Glu Cys Ser	
	445 450 455 460	
55	GGG ATC CAC AGA GAG CTG GGC GTC CAT TAC TCC CGA ATC CAG TCC CTC	1860
	Gly Ile His Arg Glu Leu Gly Val His Tyr Ser Arg Ile Gln Ser Leu	
	465 470 475	
60	ACA CTC GAC GTC CTC AGC ACC TCC GAG CTC TTG CTG GCC AAG AAC GTG	1908
	Thr Leu Asp Val Leu Ser Thr Ser Glu Leu Leu Leu Ala Lys Asn Val	
	480 485 490	

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	GGG AAT GCT GGC TTC AAT GAG ATC ATG GAG GCC TGT CTG ACG GCA GAA	1956
	Gly Asn Ala Gly Phe Asn Glu Ile Met Glu Ala Cys Leu Thr Ala Glu	
	495 500 505	
5	GAT GTG ATC AAA CCG AAT CCA GCC AGT GAC ATG CAG GCG AGG AAG GAC	2004
	Asp Val Ile Lys Pro Asn Pro Ala Ser Asp Met Gln Ala Arg Lys Asp	
	510 515 520	
10	TTT ATC ATG GCC AAA TAC ACA GAG AAA CGC TTC GCT CGT AAG AAG TGT	2052
	Phe Ile Met Ala Lys Tyr Thr Glu Lys Arg Phe Ala Arg Lys Lys Cys	
	525 530 535 540	
15	CCA GAC GCA CTG TCG AAG CTG CAC ACG CTC TGT GAT GCT GTG AAG GCC	2100
	Pro Asp Ala Leu Ser Lys Leu His Thr Leu Cys Asp Ala Val Lys Ala	
	545 550 555	
20	CGG GAC ATT TTC TCT CTC ATC CAG GTC TAT GCT GAA GGA GTG GAT CTG	2148
	Arg Asp Ile Phe Ser Leu Ile Gln Val Tyr Ala Glu Gly Val Asp Leu	
	560 565 570	
25	ATG GAG CCC ATT CCT CTG GCT AAT GGA CAT GAA CAA GGT GAG ACG GCT	2196
	Met Glu Pro Ile Pro Leu Ala Asn Gly His Glu Gln Gly Glu Thr Ala	
	575 580 585	
30	CTT CAT CTG GCC GTG AGA CTG GTG GAC AGA ACT TCC CTA CAC ATC ATC	2244
	Leu His Leu Ala Val Arg Leu Val Asp Arg Thr Ser Leu His Ile Ile	
	590 595 600	
35	GAC TTC CTC ACC CAA AAC AGT TTA AAC CTG GAT AAG CAA ACG GCT AAA	2292
	Asp Phe Leu Thr Gln Asn Ser Leu Asn Leu Asp Lys Gln Thr Ala Lys	
	605 610 615 620	
40	GGA AGC ACA GCT CTG CAT TAC TGC TGC CTG ACG GAC AAC AGC GAG TGT	2340
	Gly Ser Thr Ala Leu His Tyr Cys Cys Leu Thr Asp Asn Ser Glu Cys	
	625 630 635	
45	CTC AAA CTG CTG CTC AGA GGA AAA GCC TCC ATA GAT ATC GCT AAT GAA	2388
	Leu Lys Leu Leu Leu Arg Gly Lys Ala Ser Ile Asp Ile Ala Asn Glu	
	640 645 650	
50	GCT GGA GAG ACC CCG TTG GAC ATC GCC AGG CGA CTC AAA CAT CTG CAG	2436
	Ala Gly Glu Thr Pro Leu Asp Ile Ala Arg Arg Leu Lys His Leu Gln	
	655 660 665	
55	TGT GAG GAA CTG CTG AAC CAG GCT CTT GCA GGG AAG TTC AAT GCT CAT	2484
	Cys Glu Glu Leu Leu Asn Gln Ala Leu Ala Gly Lys Phe Asn Ala His	
	670 675 680	
60	GTG CAT GTG GAG TAT GAG TGG AGA CTT CAG CAT GAA GAC CTG GAC GAG	2532
	Val His Val Glu Tyr Glu Trp Arg Leu Gln His Glu Asp Leu Asp Glu	
	685 690 695 700	
65	AGT GAT GAA GAT CTG GAT GAG AAG TCG AGT CCT CAC CGG CGG GAT GAG	2580
	Ser Asp Glu Asp Leu Asp Glu Lys Ser Ser Pro His Arg Arg Asp Glu	
	705 710 715	

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5	CGG CCC ATC AGC TGC TAC ACA CCG GGC AGT AAC TCC CTT CAG CTG AGT	2628
	Arg Pro Ile Ser Cys Tyr Thr Pro Gly Ser Asn Ser Leu Gln Leu Ser	
	720 725 730	
10	CCA GCC AGC CTG AGC CGA GAC GGT CGA GAC CTG GTT AAA GAC AAG CAA	2676
	Pro Ala Ser Leu Ser Arg Asp Gly Arg Asp Leu Val Lys Asp Lys Gln	
	735 740 745	
15	CGC TTT GTG CCA AAC CTG GTC AAC AAT GAA ACC TAC GGG ACC ATC ATT	2724
	Arg Phe Val Pro Asn Leu Val Asn Asn Glu Thr Tyr Gly Thr Ile Ile	
	750 755 760	
20	AAC ACC AGC TCA CCC GTC AGC CTG TCC TCT TCT GCT CCA CCT CTA CCA	2772
	Asn Thr Ser Ser Pro Val Ser Leu Ser Ser Ser Ala Pro Pro Leu Pro	
	765 770 775 780	
25	CCC CGA AAC CTA GTT CAG CCG TCT GCT CTT GCA GGA CTG ACT CAA GGA	2820
	Pro Arg Asn Leu Val Gln Pro Ser Ala Leu Ala Gly Leu Thr Gln Gly	
	785 790 795	
30	TCT CCC GGC TGG AAG CCT GGC TCT CTG GAT CTG AGC GGC AGA CAG AGA	2868
	Ser Pro Gly Trp Lys Pro Gly Ser Leu Asp Leu Ser Gly Arg Gln Arg	
	800 805 810	
35	TCC TCC TCT GAC CCT CCC AAC ATG CAT CCT CCT GCG CCT CCC TTA CGG	2916
	Ser Ser Ser Asp Pro Pro Asn Met His Pro Pro Ala Pro Pro Leu Arg	
	815 820 825	
40	GTC ACT TCC ACC TCC CTT CTA ATG CCC AGC GGT GCT GCT CCT CCT CTG	2964
	Val Thr Ser Thr Ser Leu Leu Met Pro Ser Gly Ala Ala Pro Pro Leu	
	830 835 840	
45	GCT AAA GCT ACT GGT ATG ATG GAG ACC ATG AAT ATG CAA CCC AAA CCC	3012
	Ala Lys Ala Thr Gly Met Met Glu Thr Met Asn Met Gln Pro Lys Pro	
	845 850 855 860	
50	GGA CAG GGG CCT CCT GGA CAG AAC ATC AAC CGG GCT ACA AGT GCG GAC	3060
	Gly Gln Gly Pro Pro Gly Gln Asn Ile Asn Arg Ala Thr Ser Ala Asp	
	865 870 875	
55	AAA AAC TTC AGC AAA AGC ACA CTG ATG CGC TCC GGA TCC ATC GAG AGA	3108
	Lys Asn Phe Ser Lys Ser Thr Leu Met Arg Ser Gly Ser Ile Glu Arg	
	880 885 890	
60	CCA GCT AAA GAA GTC CCA GGA GGC CCA CAA AAC ACC ACT GGT CAA ACT	3156
	Pro Ala Lys Glu Val Pro Gly Gly Pro Gln Asn Thr Thr Gly Gln Thr	
	895 900 905	
65	CTG CCT GCG ACC CAC ATG CCC AGG AAA ACG TAT TTG AAG CCG AAG CGT	3204
	Leu Pro Ala Thr His Met Pro Arg Lys Thr Tyr Leu Lys Pro Lys Arg	
	910 915 920	

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	GTG AAG GCC ATG TAT AAC TGT GTG GCC GAT AAT CCA GAC GAG CTG ACC	3252
	Val Lys Ala Met Tyr Asn Cys Val Ala Asp Asn Pro Asp Glu Leu Thr	
	925 930 935 940	
5	TTC TCT GAG GGA GAG CTT ATC GTG GTG GAT GGA GAG GAG GAC CAG GAG	3300
	Phe Ser Glu Gly Glu Leu Ile Val Val Asp Gly Glu Glu Asp Gln Glu	
	945 950 955	
10	TGG TGG CTG GGC CAC ATT GAG GGA GAG CCA ATG AGA AGA GGA GCG TTT	3348
	Trp Trp Leu Gly His Ile Glu Gly Glu Pro Met Arg Arg Gly Ala Phe	
	960 965 970	
	CCT GTC ACG TTT GTA CAG TTC ATT ATG GAC TGAAGCTCGA GAGATCACAC	3398
	Pro Val Thr Phe Val Gln Phe Ile Met Asp	
15	975 980	
	ACTGAAGTGA TGACGGCACT TCTCTGCCTC TGTGTGGCCT CACTAACCAC CACTATCTTC	3458
	ATCATCATCG TTGTTCTTCC CTTTATGGTG AGGCCTGTAT CTTCAACCAAT CTTCCACAAG	3518
20	TCCTGCCTCT GGAGAAATCA GCCTTCTGGG CAATAAACGC ACTTTTGAAC TTAATTTATC	3578
	ATGAACACAA TGCTAATGAA TGTCACCAAG ATGAAGGTTT TGTTCAGGA TCATTACAT	3638
25	CCTTATTTCT TTAGACAGAT CTGTGAATAT AGTCTTATAT GCCCACATTC CACATCTGGC	3698
	AAGGAAAGAC GGAAGCATAG TAGTGAAATG ACAGCCTTTT TGGAGGACTC TGTGGGATAA	3758
	GACGGCTCTG TTAATGGTGC TAAAGCAGGA ATATGCTACA GGAGCTGTCT GTCCTAGGAG	3818
30	GAGCGCACTG ATGTCCCCGT TTTCACACTA CCTGCCCCAG TGCTGAGTGC AGAAATAGGT	3878
	TTTCTCCAGC ACTCGCACAT GGGAAATCTC TGAAGTGCAC TGTGTGATGG AGAAACTGAC	3938
35	AGACTGAAGA GTGCTTTTGC GCTGGCTGAG GGACGTGAAG ATTAAATGAA AGTAATCTTG	3998
	ACCCTGAAGC TGCTGGGATT TTGGAGCGTT GTGAATGTTT TCTGGCCTCC AGGGAAAGGA	4058
	GAGGAAGAGC ATCCAGGAGC TTTTTTTCTG TATAGGTATT TATAAATCGG AGCTGTTCTG	4118
40	TTTLAGACTC TCGTTGATTT TAACGATCTT CCGCAGAACT TGCTTCATTG TGCGAGCAAT	4178
	CTGCTGAATG ATGTCATTTT TTTTAAAGA GACAGACCAA ACCTTCAAAT AATTAATTTA	4238
45	CTCCAGGAGT GTCAAAGTTC CTGGAGGGCC ACAGCCCTGC ACAGTTTAGT TCCAACCCTG	4298
	CTCCAACACA CTTACCTGCA AGTTTCAAAC AAGCCTGAAG AACTTAATTA GTTTGATCAG	4358
	GTGTTTAATC AGGGTTGTGC AGAGCTGCGG CCCTCCAGGA ACTCAGTTTG ACACCTGTGA	4418
50	TTTACTCAAT TTACAAAATG TCCAGAGTGC TCTATATCAG CATTTCCCAA CCCTCTTCTT	4478
	GAAGGCACAC CAACAGTACA CATTTTCAAC CTCTTCCTAA GCAAACACGC CTCAATCAAC	4538
55	TCAACAGACC ATTAGAAGAG ACTCTAAAAC CTGAAGTAAA TGAGTCAGAT AAGGGAGACT	4598

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5 CCCAAAATAT GAACTGTTGG TGTGCCTCCA GGAACACTGT TTGGAAACCT TCTCTATATG 4658
 CTCAATTTGA TGTAATCCAA GTTGTCTGAA GACATACAGT AAACCTTAAAT GAGTAAATAG 4718
 ATGGGTTTTA GAGGAAAACCT AAACATTTAT TCTCAAGTCT TTACAAACCT TACTTCAGTG 4778
 TTTATTTGGA GCAATGTGGG TACTAAATGT AGGAATCTGT TCATATGGAA ATATATATAT 4838
 10 ATATATATAT ATATATATAT ATATATATAT ATTCAAAAAA GGTAATAGTG ACTTTAATCG 4898
 TACCAGTTCT GCTTATTTTA TATATGAAAG ATTTGCAACA GAAAAGTGCA AAATTGAGGT 4958
 GGCACAAATG GATTTCAATA CACTGATCCA ATTCTCTAAA TATTGTCTTA TACAATGAAA 5018
 15 TCCTACAGGA TTGTAATAGC AAATTAAGTT ATTTTCTGAA AATCATTAC TGTCATTGTC 5078
 AAACAAGGTC AAATCATCAA CTTACATTT GAATATGGAT TCAGCTTTGG TTTGAGTATT 5138
 20 CTGGTTACAG GGTGAACATG TTTCATCAAT CATACTGATT AAAGCACTCT TGCCATTTTT 5198
 CACTAATCAT CCTCTGGTTC AATGGAAGAA AAAAGTCATA CTTTGGCAT GACGGTGAGC 5258
 AAATGACAGC ATTTACATTT GTGGAGGGGG AGTGACTGTC TTTTAAGATG CTTTGCACA 5318
 25 GTTTTAAATA GAGTCTGTTT TAATTTAAAC CTTTGGATAA AAGCGTCTGC TAAATTAATA 5378
 AATTTAAACA GATTACGAAG TGTGAATGAC AGCTATTTTC TACTAGACCG TTTTGGTGTA 5438
 30 ACCCTGACGG TTGTTCCCTG TAGCAGTAAT AACTCTCTTT CTCTCTCTAG CGCTCTAATT 5498
 GTATTCCAGA GAAAATGAAA ATCTCTCTCA TCACTTCTCC TAATCCTTTG TAAAGCTCAT 5558
 CCATCAGTGA GTGTGTGCAG GAGTAACACA GCAGAGCGTT TTCTGTCAAG AGTGTTTGAT 5618
 35 GTGGTTGCAG AGCAACTTAG CGTCTGTTAT GTAACTTTTA ATTACAGTCA TGTTAGTCTT 5678
 GATTGAGCTC AGGCCAGTGT GTATACGGCC TGCACTGATT GTAAATAACT GTAGACTTTT 5738
 40 TGCTTTGTGC ATATTTAATT GTAAACAGAG AGCTAACTG ATACTGACTG ATGTGTTGAC 5798
 GTATTGTTAG ATAAGACTGT TACAGTACAC TTTTAACTAC TCACCCCTTT ACCATAAACA 5858
 TTGTTGACGC TAATATATAA TTCATATATG TACAAATAAA GAGTACTTCT AGAGCGGCCG 5918
 45 CGGGCCCATC GATTTTCCAC CCGGGTGGGT ACCAGG 5954

(2) INFORMATION FOR SEQ ID NO:7:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 982 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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5  Met Pro Asp Gln Ile Thr Val Ala Glu Phe Val Thr Glu Thr Asn Glu
   1             5             10             15

Asp Tyr Lys Ser Pro Thr Ala Ser Asn Phe Thr Thr Arg Met Thr His
           20             25             30

10 Cys Arg Asn Thr Val Ser Ala Leu Glu Glu Ala Leu Asp Val Asp Arg
    35             40             45

Ser Val Leu Tyr Lys Met Lys Lys Ser Val Lys Ala Ile Tyr Ala Ser
15  50             55             60

Gly Leu Ala His Val Glu Asn Glu Glu Gln Tyr Thr Gln Ala Leu Glu
   65             70             75             80

20 Lys Phe Gly Glu Asn Cys Val Tyr Arg Asp Asp Pro Asp Leu Gly Ser
    85             90             95

Ala Phe Leu Lys Phe Ser Val Phe Thr Lys Glu Leu Thr Ala Leu Phe
    100            105            110

25 Lys Asn Leu Phe Gln Asn Met Asn Asn Ile Ile Thr Phe Pro Leu Asp
    115            120            125

Ser Leu Leu Lys Gly Asp Leu Lys Gly Val Lys Gly Asp Leu Lys Lys
30  130            135            140

Pro Phe Asp Lys Ala Trp Lys Asp Tyr Glu Thr Lys Val Ser Lys Ile
   145            150            155            160

35 Glu Lys Glu Lys Lys Glu His Ala Arg Gln His Gly Met Ile Arg Thr
    165            170            175

Glu Ile Ser Gly Ala Glu Ile Ala Glu Glu Met Glu Lys Glu Arg Arg
    180            185            190

40 Phe Phe Gln Leu Gln Met Cys Glu Tyr Leu Leu Lys Val Asn Glu Ile
    195            200            205

Lys Ile Lys Lys Gly Val Asp Leu Leu Gln Asn Leu Ile Lys Tyr Phe
45  210            215            220

His Ala Gln Cys Asn Phe Phe Gln Asp Gly Leu Lys Ala Val Asp Asn
   225            230            235            240

50 Leu Lys Pro Ser Ile Glu Lys Leu Ala Thr Asp Leu His Ser Ile Lys
    245            250            255

Gln Val Gln Asp Glu Glu Arg Arg Gln Leu Thr Gln Leu Arg Asp Val
    260            265            270

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Leu Lys Thr Ala Leu Gln Val Glu Gln Lys Glu Asp Ser Gln Val Arg
 275 280 285

5 Gln Ser Ala Thr Tyr Ser Leu His Gln Pro Gln Gly Asn Lys Glu His
 290 295 300

Gly Thr Glu Arg Ser Gly Asn Leu Tyr Lys Lys Ser Asp Gly Leu Arg
 305 310 315 320

10 Lys Val Trp Gln Lys Arg Lys Cys Thr Val Lys Asn Gly Tyr Leu Thr
 325 330 335

Ile Ser His Gly Thr Ala Asn Arg Pro Pro Ala Lys Leu Asn Leu Leu
 340 345 350

15 Thr Cys Gln Val Lys His Asn Pro Glu Glu Lys Lys Ser Phe Asp Leu
 355 360 365

20 Ile Ser His Asp Arg Thr Tyr His Phe Gln Ala Glu Asp Glu Pro Glu
 370 375 380

Cys Gln Ile Trp Ile Ser Val Leu Gln Asn Ser Lys Glu Glu Ala Leu
 385 390 395 400

25 Asn Asn Ala Phe Lys Gly Asp Gln His Val Gly Glu Asn Asn Ile Val
 405 410 415

Gln Glu Leu Thr Lys Ala Ile Leu Gly Glu Val Lys Arg Met Ala Gly
 420 425 430

30 Asn Asp Val Cys Cys Asp Cys Gly Ala Pro Gly Pro Thr Trp Leu Ser
 435 440 445

35 Thr Asn Leu Gly Ile Leu Thr Cys Ile Glu Cys Ser Gly Ile His Arg
 450 455 460

Glu Leu Gly Val His Tyr Ser Arg Ile Gln Ser Leu Thr Leu Asp Val
 465 470 475 480

40 Leu Ser Thr Ser Glu Leu Leu Leu Ala Lys Asn Val Gly Asn Ala Gly
 485 490 495

Phe Asn Glu Ile Met Glu Ala Cys Leu Thr Ala Glu Asp Val Ile Lys
 500 505 510

45 Pro Asn Pro Ala Ser Asp Met Gln Ala Arg Lys Asp Phe Ile Met Ala
 515 520 525

50 Lys Tyr Thr Glu Lys Arg Phe Ala Arg Lys Lys Cys Pro Asp Ala Leu
 530 535 540

Ser Lys Leu His Thr Leu Cys Asp Ala Val Lys Ala Arg Asp Ile Phe
 545 550 555 560

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	Ser	Leu	Ile	Gln	Val	Tyr	Ala	Glu	Gly	Val	Asp	Leu	Met	Glu	Pro	Ile	
																	565
																	570
																	575
5	Pro	Leu	Ala	Asn	Gly	His	Glu	Gln	Gly	Glu	Thr	Ala	Leu	His	Leu	Ala	
																	580
																	585
																	590
	Val	Arg	Leu	Val	Asp	Arg	Thr	Ser	Leu	His	Ile	Ile	Asp	Phe	Leu	Thr	
																	595
																	600
																	605
10	Gln	Asn	Ser	Leu	Asn	Leu	Asp	Lys	Gln	Thr	Ala	Lys	Gly	Ser	Thr	Ala	
																	610
																	615
																	620
	Leu	His	Tyr	Cys	Cys	Leu	Thr	Asp	Asn	Ser	Glu	Cys	Leu	Lys	Leu	Leu	
																	625
																	630
																	635
15	Leu	Arg	Gly	Lys	Ala	Ser	Ile	Asp	Ile	Ala	Asn	Glu	Ala	Gly	Glu	Thr	
																	645
																	650
																	655
20	Pro	Leu	Asp	Ile	Ala	Arg	Arg	Leu	Lys	His	Leu	Gln	Cys	Glu	Glu	Leu	
																	660
																	665
																	670
	Leu	Asn	Gln	Ala	Leu	Ala	Gly	Lys	Phe	Asn	Ala	His	Val	His	Val	Glu	
																	675
																	680
																	685
25	Tyr	Glu	Trp	Arg	Leu	Gln	His	Glu	Asp	Leu	Asp	Glu	Ser	Asp	Glu	Asp	
																	690
																	695
																	700
	Leu	Asp	Glu	Lys	Ser	Ser	Pro	His	Arg	Arg	Asp	Glu	Arg	Pro	Ile	Ser	
																	705
																	710
																	715
30	Cys	Tyr	Thr	Pro	Gly	Ser	Asn	Ser	Leu	Gln	Leu	Ser	Pro	Ala	Ser	Leu	
																	725
																	730
																	735
35	Ser	Arg	Asp	Gly	Arg	Asp	Leu	Val	Lys	Asp	Lys	Gln	Arg</				

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850 855 860

Pro Gly Gln Asn Ile Asn Arg Ala Thr Ser Ala Asp Lys Asn Phe Ser
865 870 875 880

5 Lys Ser Thr Leu Met Arg Ser Gly Ser Ile Glu Arg Pro Ala Lys Glu
 885 890 895

Val Pro Gly Gly Pro Gln Asn Thr Thr Gly Gln Thr Leu Pro Ala Thr
10 900 905 910

His Met Pro Arg Lys Thr Tyr Leu Lys Pro Lys Arg Val Lys Ala Met
 915 920 925

15 Tyr Asn Cys Val Ala Asp Asn Pro Asp Glu Leu Thr Phe Ser Glu Gly
 930 935 940

Glu Leu Ile Val Val Asp Gly Glu Glu Asp Gln Glu Trp Trp Leu Gly
20 945 950 955 960

His Ile Glu Gly Glu Pro Met Arg Arg Gly Ala Phe Pro Val Thr Phe
 965 970 975

Val Gln Phe Ile Met Asp
25 980

(2) INFORMATION FOR SEQ ID NO:8:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2949 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGCCTGACC AGATAACAGT GCGGAGTTT GTCACGGAGA CAAATGAAGA TTATAAATCG 60

CCCACCGCCT CAAACTTCAC CACCAGAATG ACTCACTGCA GGAACACAGT ATCCGCACTG 120

45 GAGGAGGCCC TGGATGTGGA CCGCAGTGTC CTTTACAAGA TGAAGAAGTC AGTTAAGGCT 180

ATTTACGCCT CGGGTCTGGC TCATGTGGAG AATGAGGAGC AGTACACTCA AGCTCTGGAG 240

AAGTTCTGGAG AGAACTGTGT GTACAGAGAT GACCCGGACC TGGGATCAGC CTTCTGAAG 300

50 TTCTCCGTCT TCACCAAGGA GCTCAGGCA CTCTTCAAGA ACCTGTTTCA GAACATGAAT 360

AATATCATTA CCTTCCATT GGACAGTCTG CTGAAGGGAG ATCTGAAAGG GGTAAAGGG 420

55 GATCTCAAGA AGCCCTTCGA TAAAGCCTGG AAAGACTACG AGACTAAAGT CTCTAAATA 480

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GAGAAGGAGA AAAAAGAGCA CGCCCGGCAG CACGGAATGA TCCGGACGGA GATCAGCGGA 540
 GCAGAGATAG CAGAAGAGAT GGAAAAAGAG CGGCGTTTCT TCCAGCTTCA GATGTGTGAG 600
 5 TACCTCCTCA AAGTCAATGA AATCAAGATC AAAAAAGGTG TCGACCTGCT CCAGAATCTC 660
 ATCAAATACT TCCACGCACA GTGCAACTTC TTTCAGGATG GTCTCAAAGC GGTGGACAAC 720
 10 CTCAAACCCT CAATAGAAAA ACTGGCCACA GACTTGCACT CGATCAAACA GGTACAGGAT 780
 GAAGAACGCA GACAGCTAAC CCAGTTACGG GATGTGCTAA AACTGCTCT GCAAGTGGAG 840
 CAGAAGGAGG ACTCTCAGGT TAGACAGAGC GCCACCTACA GTCTGCACCA GCCGCAGGGC 900
 15 AACAAAGAGC ATGGGACTGA GCGCAGCGGC AACCTTTACA AGAAGAGTGA CGGGCTGCGG 960
 AAAGTGTGGC AGAAGAGAAA GTGCACAGTA AAGAATGGAT ATTTGACCAT CTCACATGGG 1020
 20 ACGGCAAACA GACCTCCCGC CAACTCAAT CTTCTCACCT GTCAGGTGAA GCACAACCCA 1080
 GAGGAGAAGA AAAGTTTTGA CCTCATCTCA CATGACAGAA CATATCATTT CCAGGCAGAA 1140
 GATGAGCCAG AGTGTCAAAT ATGGATCTCA GTGCTGCAGA ACAGTAAAGA AGAGGCGCTC 1200
 25 AACACGCCT TCAAGGGCGA CCAGCATGTT GGTGAAAATA ACATTGTGCA GGAGCTCACC 1260
 AAGGCCATCC TGGGAGAGGT GAAGCGGATG GCGGGGAACG ATGTCTGCTG CGACTGCGGT 1320
 30 GCTCCCGGCC CCACATGGCT CTCCACCAAC CTGGGCATCC TGACCTGCAT CGAGTGTTCTG 1380
 GGGATCCACA GAGAGCTGGG CGTCCATTAC TCCGAATCC AGTCCCTCAC ACTCGACGTC 1440
 CTCAGCACCT CCGAGCTCTT GCTGGCCAAG AACGTGGGGA ATGCTGGCTT CAATGAGATC 1500
 35 ATGGAGGCCT GTCTGACGGC AGAAGATGTG ATCAAACCGA ATCCAGCCAG TGACATGCAG 1560
 GCGAGGAAGG ACTTTATCAT GGCCAAATAC ACAGAGAAAC GCTTCGCTCG TAAGAAGTGT 1620
 40 CCAGACGCAC TGTCGAAGCT GCACACGCTC TGTGATGCTG TGAAGGCCCG GGACATTTTC 1680
 TCTCTCATCC AGGTCTATGC TGAAGGAGTG GATCTGATGG AGCCATTCC TCTGGCTAAT 1740
 GGACATGAAC AAGGTGAGAC GGCTCTTCAT CTGGCCGTGA GACTGGTGGA CAGAACTTCC 1800
 45 CTACACATCA TCGACTTCCT CACCCAAAAC AGTTTAAACC TGGATAAGCA AACGGCTAAA 1860
 GGAAGCACAG CTCTGCATTA CTGCTGCCTG ACGGACAACA GCGAGTGTCT CAAACTGCTG 1920
 50 CTCAGAGGAA AAGCCTCCAT AGATATCGCT AATGAAGCTG GAGAGACCCC GTTGGACATC 1980
 GCCAGGCGAC TCAAACATCT GCAGTGTGAG GAACTGCTGA ACCAGGCTCT TGCAGGGAAG 2040
 55 TTCAATGCTC ATGTGCATGT GGAGTATGAG TGGAGACTTC AGCATGAAGA CCTGGACGAG 2100

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AGTGATGAAG ATCTGGATGA GAAGTCGAGT CCTCACC GGC GGGATGAGCG GCCCATCAGC 2160
TGCTACACAC CGGGCAGTAA CTCCCTTCAG CTGAGTCCAG CCAGCCTGAG CCGAGACGGT 2220
5 CGAGACCTGG TTAAAGACAA GCAACGCTTT GTGCCAAACC TGGTCAACAA TGAAACCTAC 2280
GGGACCATCA TTAACACCAG CTCACCCGTC AGCCTGTCCT CTTCTGCTCC ACCTCTACCA 2340
10 CCCCAGAAACC TAGTTCAGCC GTCTGCTCTT GCAGGACTGA CTCAAGGATC TCCCGGCTGG 2400
AAGCCTGGCT CTCTGGATCT GAGCGGCAGA CAGAGATCCT CCTCTGACCC TCCCAACATG 2460
CATCCTCCTG CGCCTCCCTT ACGGGTCACT TCCACCTCCC TTCTAATGCC CAGCGGTGCT 2520
15 GCTCCTCCTC TGGCTAAAGC TACTGGTATG ATGGAGACCA TGAATATGCA ACCCAAACCC 2580
GGACAGGGGC CTCCTGGACA GAACATCAAC CGGGCTACAA GTGCGGACAA AAACCTTCAGC 2640
AAAAGCACAC TGATGCGCTC CGGATCCATC GAGAGACCAG CTAAAGAAGT CCCAGGAGGC 2700
20 CCACAAAACA CCACTGGTCA AACTCTGCCT GCGACCCACA TGCCCAGGAA AACGTATTTG 2760
AAGCCGAAGC GTGTGAAGGC CATGTATAAC TGTGTGGCCG ATAATCCAGA CGAGCTGACC 2820
25 TTCTCTGAGG GAGAGCTTAT CGTGGTGGAT GGAGAGGAGG ACCAGGAGTG GTGGCTGGGC 2880
CACATTGAGG GAGAGCCAAT GAGAAGAGGA GCGTTTCCTG TCACGTTTGT ACAGTTCATT 2940
ATGGACTGA 2949

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 4595 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40

(ix) FEATURE:

- 45 (A) NAME/KEY: CDS
(B) LOCATION: 300..3008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

50 GGAGCTCGCG CGCCTGCAGG TCGACACTAG TGGATCCAAA GAATTCGGCA CGAGCAGAAG 60
TGTTGATCTT GTCAGCTGCT CGTGTGATGG AGTTGTTTAA CGCTTGTGTT CAAAGGCAAA 120
TCCTCTCCTC ATCGGCCGTT TACATTTTAA CTTACGCGG AAATTTAAAA CTGAACATAAT 180
55 CTCTAAGGAA TGAAGTAAAT GGACTTGAGT TGAAGTCTGG TTTTGTAGCG CGAAGCTACA 240

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ACTTTAAGCA AACTTTCTTT CTTTTTGGGA TCTATTGTGT AGATTTAAAA GGAATAATC 299
 5 ATG CCT GAT CAG CTG ACA GTG ACT GAG TTT GTG GAT ATT ACC CAT GAG 347
 Met Pro Asp Gln Leu Thr Val Thr Glu Phe Val Asp Ile Thr His Glu
 1 5 10 15
 10 GAC TAT AAA GCA CCG ACA ACA TCA GTG TTC TGC ACG CGC ATG GCT CAC 395
 Asp Tyr Lys Ala Pro Thr Thr Ser Val Phe Cys Thr Arg Met Ala His
 20 25 30
 15 TGC AGG AAT ACA GTC GCC GCT CTG GAA GAG GCG CTG GAT CTG GAC CGC 443
 Cys Arg Asn Thr Val Ala Ala Leu Glu Glu Ala Leu Asp Leu Asp Arg
 35 40 45
 AGT GTA CTG CAC AAA ATG AAG AAG TCA GTC AAG GCC ATA AAC AGC TCT 491
 Ser Val Leu His Lys Met Lys Lys Ser Val Lys Ala Ile Asn Ser Ser
 50 55 60
 20 GGT CAG ACT CAT GTA GAG AAC GAG GAG CAG TAC ATC CAG GCC ATA GAG 539
 Gly Gln Thr His Val Glu Asn Glu Glu Gln Tyr Ile Gln Ala Ile Glu
 65 70 75 80
 25 AGG TTT ACG GAT AAC ACT GTG TAC AAA GAT GAC CCT GAG ATG TCC AAT 587
 Arg Phe Thr Asp Asn Thr Val Tyr Lys Asp Asp Pro Glu Met Ser Asn
 85 90 95
 30 TAC TTC CTC ACA TTC GCT GGT TTC ACC AAG GAG CTT ACT GCT CTT TTC 635
 Tyr Phe Leu Thr Phe Ala Gly Phe Thr Lys Glu Leu Thr Ala Leu Phe
 100 105 110
 AAG AAC TTG CTA CAG AAC ATG AAT AAC ATC ATC ACT TTT CCA CTA GAC 683
 Lys Asn Leu Leu Gln Asn Met Asn Asn Ile Ile Thr Phe Pro Leu Asp
 115 120 125
 35 AGT CTG CTA AAG GGA GAC CTC AAA GGA GTC AAA GGG GAT TTG AAA AAG 731
 Ser Leu Leu Lys Gly Asp Leu Lys Gly Val Lys Gly Asp Leu Lys Lys
 130 135 140
 40 CCA TTT GAT AAA GCA TGG AAG GAT TAT GAA ACC AAA CTG AGC AAG ATT 779
 Pro Phe Asp Lys Ala Trp Lys Asp Tyr Glu Thr Lys Leu Ser Lys Ile
 145 150 155 160
 45 GAG AAA GAA AAG CGA GAA CAT GCC AAA CAG CAC GGT CTG ATC CGA ACA 827
 Glu Lys Glu Lys Arg Glu His Ala Lys Gln His Gly Leu Ile Arg Thr
 165 170 175
 GAG ATC AGT GGA GGA GAG ATC GCA GAA GAG ATG GAG AAA GAG AGA CGC 875
 Glu Ile Ser Gly Gly Glu Ile Ala Glu Glu Met Glu Lys Glu Arg Arg
 180 185 190
 50 CTG TTT CAG CTT CAG ATG TGT GAG TAC CTC ATT AAA GTG AAT GAA ATC 923
 Leu Phe Gln Leu Gln Met Cys Glu Tyr Leu Ile Lys Val Asn Glu Ile
 195 200 205
 55

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	AAA GTC AAA AAG GGG GTC GAC CTG CTT CAC AAC CTC ATC AAA TAC TTT	971
	Lys Val Lys Lys Gly Val Asp Leu Leu His Asn Leu Ile Lys Tyr Phe	
	210 215 220	
5	CAT GCC CAG TGC AAT TTC TTT CAG GAT GGG CTA AAG GTC GTG GAC AAT	1019
	His Ala Gln Cys Asn Phe Phe Gln Asp Gly Leu Lys Val Val Asp Asn	
	225 230 235 240	
10	CTG AAA CCT TTC ATG GAA AAG CTT GCC ACA GAC TTA ACC GCG AAC AAA	1067
	Leu Lys Pro Phe Met Glu Lys Leu Ala Thr Asp Leu Thr Ala Asn Lys	
	245 250 255	
15	CAG ACT CAA GAT GCA GAA AGG AAA CAG TTG CTG CAG CTG AAA GAA ACT	1115
	Gln Thr Gln Asp Ala Glu Arg Lys Gln Leu Leu Gln Leu Lys Glu Thr	
	260 265 270	
20	CTT AAA TCT GCT CTA CAG TCT GAG TGT AAG GAG GAT GCT CAG TCA AAG	1163
	Leu Lys Ser Ala Leu Gln Ser Glu Cys Lys Glu Asp Ala Gln Ser Lys	
	275 280 285	
	CAG AAC GCA GGC TAC AGT CTT CAC CAG TTG CAG GGC AAT AAA GCT CAC	1211
	Gln Asn Ala Gly Tyr Ser Leu His Gln Leu Gln Gly Asn Lys Ala His	
	290 295 300	
25	GGC ACG GAG CGC TCT GGG ATG CTC CTC AAA CGC AGC GAG GGA CTG AGG	1259
	Gly Thr Glu Arg Ser Gly Met Leu Leu Lys Arg Ser Glu Gly Leu Arg	
	305 310 315 320	
30	AAA GTT TGG CAG AAA AGG AAG TGC TCT GTG AAA AAT GGA TTG TTG ACT	1307
	Lys Val Trp Gln Lys Arg Lys Cys Ser Val Lys Asn Gly Leu Leu Thr	
	325 330 335	
35	ATT TCA CAT GGA ACG CCC AAT GCA CCG CCA GCA AAC CTG AAC CTC TTA	1355
	Ile Ser His Gly Thr Pro Asn Ala Pro Pro Ala Asn Leu Asn Leu Leu	
	340 345 350	
40	ACC TGC CAA GTG AAG CGT AAC CCA GAT GAG AAA AAA TGC TTT GAT CTC	1403
	Thr Cys Gln Val Lys Arg Asn Pro Asp Glu Lys Lys Cys Phe Asp Leu	
	355 360 365	
	ATA TCA CAT GAC AGA ACG TAT CAC TTC CAG ACT GAG GAT GAG GCA GAG	1451
	Ile Ser His Asp Arg Thr Tyr His Phe Gln Thr Glu Asp Glu Ala Glu	
	370 375 380	
45	TGT CAG GTA TGG GTT TCT GTT CTC CAG AAC AGT AAA GAA GAG GCG CTG	1499
	Cys Gln Val Trp Val Ser Val Leu Gln Asn Ser Lys Glu Glu Ala Leu	
	385 390 395 400	
50	AAC AAT GCC TTT AAA GAC GAT CAG AAT GAG GGA GAA AAT AAC ATT GTT	1547
	Asn Asn Ala Phe Lys Asp Asp Gln Asn Glu Gly Glu Asn Asn Ile Val	
	405 410 415	
55	CGA GAG CTC ACT AAG GCC ATC GTG GGG GAA GTG AAG AAA ATG AGC GGC	1595
	Arg Glu Leu Thr Lys Ala Ile Val Gly Glu Val Lys Lys Met Ser Gly	
	420 425 430	

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	AAT GAC GTG TGC TGT GAC TGT GGA GCT TCC AAT CCA ACA TGG CTC TCC	1643
	Asn Asp Val Cys Cys Asp Cys Gly Ala Ser Asn Pro Thr Trp Leu Ser	
	435 440 445	
5	ACA AAC CTG GGT GTG TTG ATT TGC ATT GAA TGC TCT GGG ATC CAT CGG	1691
	Thr Asn Leu Gly Val Leu Ile Cys Ile Glu Cys Ser Gly Ile His Arg	
	450 455 460	
10	GAA ATG GGC GTC CAC TAC TCC CGA ATA CAG TCT CTG ACA CTG GAC CTC	1739
	Glu Met Gly Val His Tyr Ser Arg Ile Gln Ser Leu Thr Leu Asp Leu	
	465 470 475 480	
15	TTA GGC ACA TCT GAA CTA TTG CTT GCT AAC AGT GTG GGA AAT GCA GCA	1787
	Leu Gly Thr Ser Glu Leu Leu Leu Ala Asn Ser Val Gly Asn Ala Ala	
	485 490 495	
20	TTC AAT GAA ATC ATG GAA GCA AAA CTG TCT TCA GAG ATC CCA AAA CCC	1835
	Phe Asn Glu Ile Met Glu Ala Lys Leu Ser Ser Glu Ile Pro Lys Pro	
	500 505 510	
	TAC CCT TCT AGT GAC ATG CAG GTA CGA AAA GAC TTC ATC ACA GCC AAA	1883
	Tyr Pro Ser Ser Asp Met Gln Val Arg Lys Asp Phe Ile Thr Ala Lys	
	515 520 525	
25	TAC ACA GAG AAG CGT TTC GCT CAG AAG AAG TAT GCA GAT AAC GCA GCT	1931
	Tyr Thr Glu Lys Arg Phe Ala Gln Lys Lys Tyr Ala Asp Asn Ala Ala	
	530 535 540	
30	CGA CTG CAT GCA CTG TGT GAT GCA GTG AAG TCT CGG GAC ATC TTC TCC	1979
	Arg Leu His Ala Leu Cys Asp Ala Val Lys Ser Arg Asp Ile Phe Ser	
	545 550 555 560	
35	CTG ATC CAG GTC TAT GCT GAA GGA CTG GAC CTG ATG GAG ACC ATT AAT	2027
	Leu Ile Gln Val Tyr Ala Glu Gly Leu Asp Leu Met Glu Thr Ile Asn	
	565 570 575	
40	CAG CCT AAC CAA CAT GAA CCA GGC GAG ACA TCA CTA CAT CTT GCG GTA	2075
	Gln Pro Asn Gln His Glu Pro Gly Glu Thr Ser Leu His Leu Ala Val	
	580 585 590	
	CGA ATG GTG GAC CGA AAC TCC CTC CAT ATT GTG GAC TTT CTT GTA CAG	2123
	Arg Met Val Asp Arg Asn Ser Leu His Ile Val Asp Phe Leu Val Gln	
	595 600 605	
45	AAC AGT GGC AAT TTA GAC AAG CAG ACA GCC AAA GGA AGC ACA GCG CTA	2171
	Asn Ser Gly Asn Leu Asp Lys Gln Thr Ala Lys Gly Ser Thr Ala Leu	
	610 615 620	
50	CAT TAT TGC TGC TTG ACT GAT AAC AGT GAA TGT ATG AAG CTG CTG CTG	2219
	His Tyr Cys Cys Leu Thr Asp Asn Ser Glu Cys Met Lys Leu Leu Leu	
	625 630 635 640	

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	CGG GGG AAA GCA TCT GTC AGC ATT ACT AAT GAT GCT GGA GAG ACT GCT	2267
	Arg Gly Lys Ala Ser Val Ser Ile Thr Asn Asp Ala Gly Glu Thr Ala	
	645 650 655	
5	CTG GAT TTG GCG CAG CGT CTC AAA CAC TCC AAA TGC GAG GAG CTG CTG	2315
	Leu Asp Leu Ala Gln Arg Leu Lys His Ser Lys Cys Glu Glu Leu Leu	
	660 665 670	
10	ACT CAG GCG CAG ACG GGG AAG TTC AAT GTC CAT GTG CAT GTG GAA TAT	2363
	Thr Gln Ala Gln Thr Gly Lys Phe Asn Val His Val His Val Glu Tyr	
	675 680 685	
15	GAC TGG CGT CTG CAT AAT GAG GAT CTG GAC GAG AGC GAA GAT GAG ATG	2411
	Asp Trp Arg Leu His Asn Glu Asp Leu Asp Glu Ser Glu Asp Glu Met	
	690 695 700	
20	GAG GAC AAG CCC ATT CCC ATC AGG CGT GAG GAG CGT CCA ATA AGC TGT	2459
	Glu Asp Lys Pro Ile Pro Ile Arg Arg Glu Glu Arg Pro Ile Ser Cys	
	705 710 715 720	
	ATA GTT CCA GGC AGT GGC CCC ATG ATG CCC AAC ATG AGC GCT CTG GCT	2507
	Ile Val Pro Gly Ser Gly Pro Met Met Pro Asn Met Ser Ala Leu Ala	
	725 730 735	
25	CGG GAC GTG GCC AAT GTG GTC AAT AAT AAG CAG AGG GCT TTT ATT CCG	2555
	Arg Asp Val Ala Asn Val Val Asn Asn Lys Gln Arg Ala Phe Ile Pro	
	740 745 750	
30	AGC ATG ATG ATG AAC GAG ACT TAC GGC ACC ATG CTC GAT CCC AAC TCT	2603
	Ser Met Met Met Asn Glu Thr Tyr Gly Thr Met Leu Asp Pro Asn Ser	
	755 760 765	
35	CCA CCA CTG GGT TTA CCA GGA GTA CCT GGC ATT CCT CTT TTA CCC CCT	2651
	Pro Pro Leu Gly Leu Pro Gly Val Pro Gly Ile Pro Leu Leu Pro Pro	
	770 775 780	
40	CGG CCC TTG GGA AGG GGA TGG AGT CCA CCA ATG GAG AAC ATC GGT AGA	2699
	Arg Pro Leu Gly Arg Gly Trp Ser Pro Pro Met Glu Asn Ile Gly Arg	
	785 790 795 800	
	CAG AGG TCA TGT TCA GAT CCT GCA AAC CCT CAA ACT CCT GAA CAA AAT	2747
	Gln Arg Ser Cys Ser Asp Pro Ala Asn Pro Gln Thr Pro Glu Gln Asn	
	805 810 815	
45	AAC TCT GTG TAT GTT CTG CCT CCT GCT CCT CCA CCT CCT CCT GCA CCC	2795
	Asn Ser Val Tyr Val Leu Pro Pro Ala Pro Pro Pro Pro Pro Ala Pro	
	820 825 830	
50	AAG AGA CCT CCA CCT CCA GAT CCA AAG GCC AGT CTT CTT CCT CCA GCA	2843
	Lys Arg Pro Pro Pro Pro Asp Pro Lys Ala Ser Leu Leu Pro Pro Ala	
	835 840 845	
55	GCC ACG GCT CCT CCT GCA CCA TCC GCA CCG CTC CTT ATT CCA CCT GCT	2891
	Ala Thr Ala Pro Pro Ala Pro Ser Ala Pro Leu Leu Ile Pro Pro Ala	
	850 855 860	

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5	CCT CTC AGG CCA GCG CCT GTA GTG CCC CCT GCA CCA GTT ATG CCC ACT	2939
	Pro Leu Arg Pro Ala Pro Val Val Pro Pro Ala Pro Val Met Pro Thr	
	865 870 875 880	
10	TCG TCA CTG ACT GAT GTC AAA AGT CTG CTG TCT AAA GCC CAG CTC ACA	2987
	Ser Ser Leu Thr Asp Val Lys Ser Leu Leu Ser Lys Ala Gln Leu Thr	
	885 890 895	
15	TTG TGC GAT TTC GAA TAC TAC TAAATGATTG TAGCATCAGA GTGCACAAGT	3038
	Leu Cys Asp Phe Glu Tyr Tyr	
	900	
20	ATGATCCGCA TGTGTCCCTC AGTTTTCATA ATGTCAGATT GAACCACAGT TAAGATGCAC	3098
	CAAACATGGA CACGCAAGAA AACTCACCCCT GGAGTTTGGC ATCATCCATC TGTGACACCT	3158
	TCACTCTACT GCATCCTGAC ATGAAACCTC ACGGTAAACA TAAACAACT GTAGCAACAC	3218
25	TTTACTTAC AACACGTCTC AGTGATAACC GGAAAAGGCA GTGGTTTGAA AGTGTCGTTT	3278
	TGATTGCGTC ATCAGATATA CCGCTCCTAT TGATTCTTGG TTAGACGCTC GTCTTAACTG	3338
	AATTCACACT TCAGCCAAGA GTCTGAACGC CCGACACCAC CAGAACTTCT TCATCAGAGG	3398
30	GAAAATCTGA TCGTAGAGGC CATCAATCAA GGAATCAAAA ACTACAGATT TTAGGCTAGG	3458
	ATTACTGGAA TCTTTTAGGA TTTTCCATAT TAGTCTCAGA TGGCCAAATC ATCTCTGAAA	3518
	TTGCACAGTG TGAGCAGGGC TTAAATCAGA TCACCAAACCT ATTGTTGAGA CCTAACACCA	3578
35	CTGAATATTT AACAAATCAAT ACACCCCTCA GCCATCCGTG TGGCTAATTG GTGGTGTACG	3638
	AGACATTCAC AAGCATTAAG ACCTCAGGAA GTGTTACTTT GATTACTTTG ATTCTAAGTG	3698
	CAATTACCTC TACCTTTAAT ACGGAAATCG TTTATGAACT GTGATGAGTG ATATGCATTA	3758
40	TACGGGGACG GTTTGGTTTT ATTAAGCGAG ATGTGGTTGG ATGAGCTTTT TGTGTTTTTC	3818
	AGACAGCAGT GGCAGAGTGA CTCCTATTTG GCAAGTGTTT AAAGGCACAA TATGTAATAT	3878
	TCACCACAAG GGGGCACATA TTCACAACAA ACAAATGGTT ATGTCTGTTA GGGTGCTGCA	3938
45	CTTTGCAGTG TAATAAAACG CACAACATTT TAAAGCGTCT TTGGAGTTTT TCTGTTTTCT	3998
	AGAAAACCAA ACTAGAAATC GAAGGTGATG AGCAACTGGA AAATGCAGGT GTATGATGTC	4058
	ATAAGCATGG AGACACTAGT TAAAATAACT TATATCTCTG GATTTGAACA TTCTTCCTAA	4118
50	CCTTTGGGAT AATGCAAGTA CTCAGCCAA AATATATCAC ACTGTTTTAG TGATTTTAGG	4178
	ATATTTGAAA GAAAATAATC GTACATATTG TGCCTTTAAG TAACATGATG AACCAGGTAG	4238
	GTTGCTTCTC AAGATTTGTT ACCAGACAAG CCATTAACT TACTCTGCTT CATTTTCAGC	4298
55		

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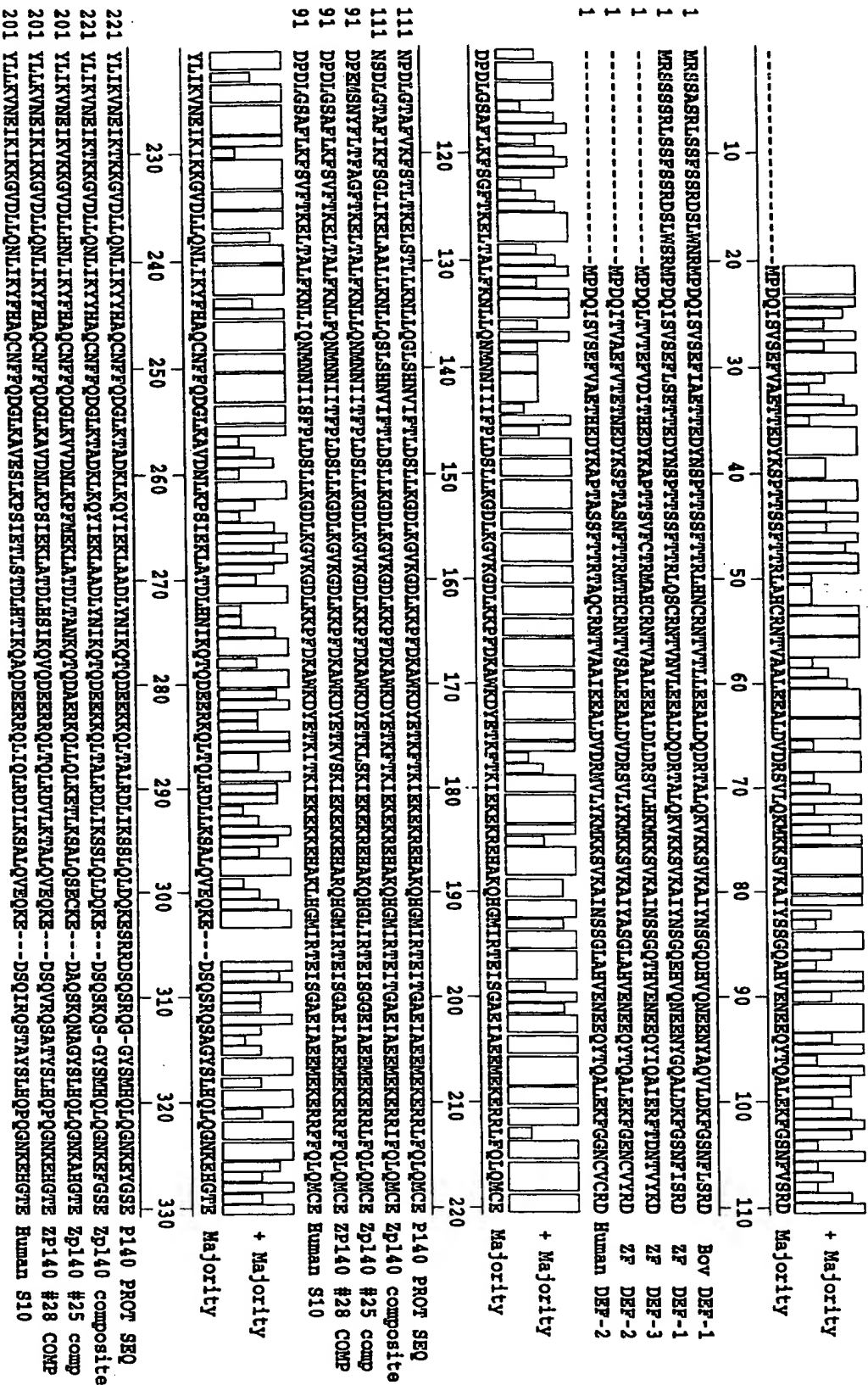


Fig. 12

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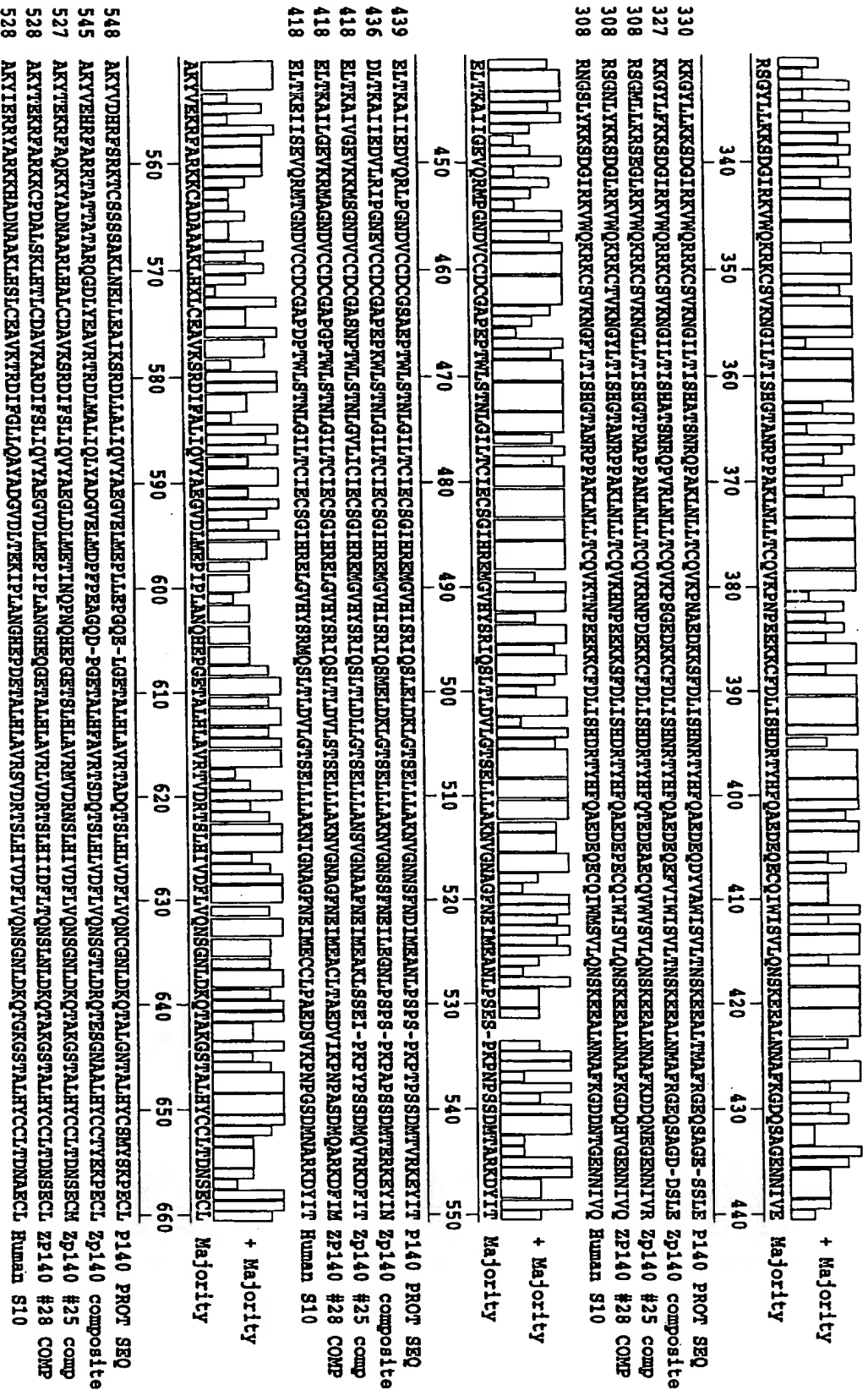


Fig. 12 CONTINUED

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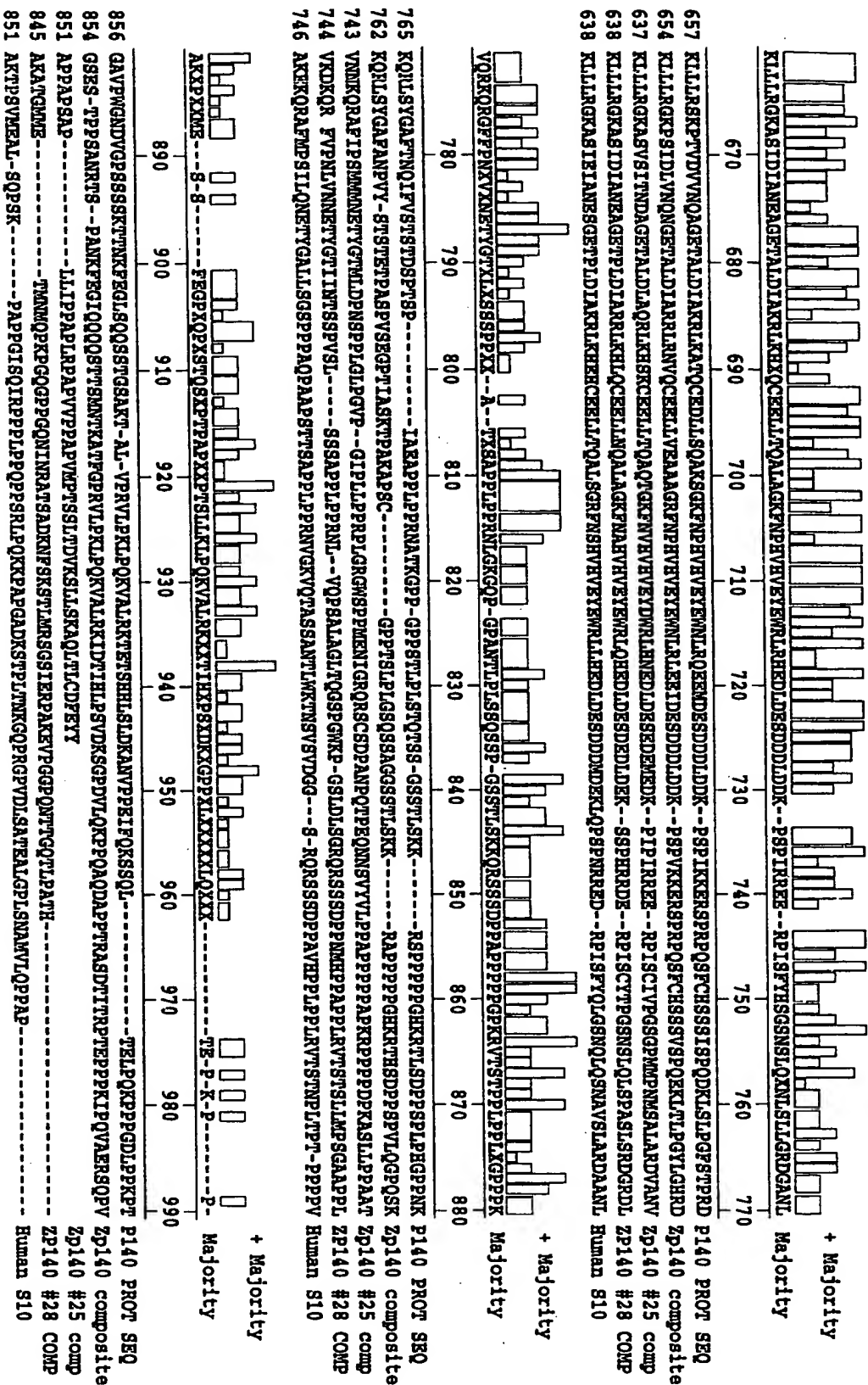


Fig. 12 CONTINUED

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Fig. 12 CONTINUED